

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 8, 2002, 06:47:02 ; Search time 2892.64 Seconds  
(without alignments)  
2958.221 Million cell updates/sec

Title: US-09-503-596-2  
Perfect score: 634  
Sequence: 1 ggaattccaggagggtgcag.....ataacttttttagatttag 634

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	607.6	95.8	628	10	BG286487
2	601.4	94.9	635	9	AA843663
3	598.6	94.4	636	10	BG570228
4	598.4	94.4	632	10	BG288820
5	597.4	94.2	620	9	AT635512
6	597.2	94.2	903	10	BG434107
7	596.4	94.1	630	9	AT652163
8	596.4	94.0	635	9	AT651387
9	590.4	93.1	637	9	AL047557
10	588.8	92.9	678	10	BG287253
11	586	92.4	616	9	AW237388
12	585	92.3	900	10	BG261014
13	584.2	92.2	632	10	BG289969
14	584.2	92.1	608	10	BE379934
15	582.8	91.9	654	10	BG287532
16	581.6	91.7	886	10	BG622132
17	577	91.0	905	10	BG572115

18	573.2	90.4	633	10	BG290820
19	561.8	88.6	682	10	BG261077
20	558	88.0	612	10	BG288203
21	556.6	87.8	597	9	AW236921
22	553	87.2	589	10	BE56868
23	550.4	86.8	591	9	AA732844
24	544.8	85.9	776	10	BI821655
25	542.8	85.6	576	9	AA777211
26	537.6	84.8	554	10	BE549708
27	528.4	83.3	570	9	AL047558
28	524	82.6	571	9	AI192168
29	521.8	82.3	559	9	AW051840
30	517	81.5	545	10	BF434751
31	515.8	81.4	767	10	BG289936
32	514.6	81.2	777	10	BF027862
33	513.6	81.0	621	10	BG285906
34	512.6	80.9	539	10	BG655515
35	511	80.6	560	9	AA861653
36	509	80.3	527	10	BG542023
37	508	80.1	542	10	BF590882
38	507.8	80.1	548	9	AI194006
39	500.4	78.9	619	10	BG285965
40	493	77.8	559	10	BE566213
41	492.8	77.7	505	9	AW631118
42	491.8	77.6	505	9	AT767352
43	491.6	77.5	524	9	AW241575
44	491.4	77.5	855	10	BE568599
45	488.8	77.1	606	9	AA126737

## ALIGNMENTS

RESULT 1

LOCUS BG286487 628 bp mRNA linear EST 21-FEB-2001  
DEFINITION 602382975F1 NIH\_MGC\_93 Homo sapiens cDNA clone IMAGE:4500475 5', mRNA sequence.

ACCESSION BG286487  
VERSION BG286487.1 GI:13039399

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 628)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-re@mail.nih.gov](mailto:cgapbs-re@mail.nih.gov)

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Cloned by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM10366 row: e column: 20

High quality sequence stop: 610.

FEATURES

Location/Qualifiers

1..628

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:4500475"

/clone.lib="NIH\_MGC\_93"

/tissue.type="transitional cell papilloma, cell line"

/lab.host="DH10B (phage-resistant)"

/note="Organ: bladder; Vector: pCMV-SPORT6; Site:1: NotI; Site:2: SalI; Cloned unidirectionally; oligo-dt primed.

Average insert size 1.7 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH\_MGC Library."

BASE COUNT 208 a 107 c 141 g 172 t  
ORIGIN

Query Match 95.8%; Score 607.6; DB 10; Length 628;  
Best Local Similarity 99.3%; Pred. No. 3e-153;  
Matches 610; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 20 gcttctctcacccttgaggaataatcctcagtaaaactcacaaaatgtgtgctcttctgt 79  
Db 1 GCTTCCTCTCACCTTGGAAGATAATCTAGAAAACCTACAAAATGTGTGATGCTTTTGT 60

Qy 80 aggtacctggaacttctcctcagtgaaacttttgatgattatgaagaagttaggagt 139  
Db 61 AGGTACCTGGAACTTGTCTCCAGTGAAGAACTTTGATGATTATGAAAGAGTAGGAGT 120

Qy 140 gggcttgcaccaggaagtggtgcatggcgaacaaactaacatgatcatcagtgtaa 199  
Db 121 GGGCTTTGCCACCAAGGAAGTGGCTGGCATGGCCAAACCTAACATGATCATCAGTGTGAA 180

Qy 200 tgggatgtgatcaccattaaatctgaaagtcacttttaaaatactgagatttccctcat 259  
Db 181 TGGGGATGTGATCACCATTAAATCTGAAAGTACCTTTTAAATACTGAGATTTCCTTCAT 240

Qy 260 actgggcccaggaatttgacgaagtcactgcagatgacaggaagtcaagacacataac 319  
Db 241 ACTGGCCAGGAATTTGACGAAGTCACTGCGATGACAGGAAAGTCAAGAGCACCATAAC 300

Qy 320 cttagatgggggtgtcctgtacatgtcagaaatggatgaaatacaacacacataaa 379  
Db 301 CTTAGATGGGGGTGCTCGGTACATGTGCAGAAATGGATGGAATAACACACCATAAA 360

Qy 380 gagaaacagagagatgataaactggtgtggaatgcctcatgaaagcgtcactccac 439  
Db 361 GAGAAAACGAGAGATGATAAATGTTGGTGAATGCGTCATGAAAGCGTCACCTCCAC 420

Qy 440 gagagtttatgagagagataagcaagggagcgttgacctggaactggaagtcgcatgaa 499  
Db 421 GAGAGTTTATGAGAGAGATTAAGCAAGGACGTTGACCTGGACTGAAGTTGCGATTGAA 480

Qy 500 ctctacaacattctgtggatatattgtcacaagaatattgttttccctcaatttag 559  
Db 481 CTCACACACATCTGTGGGATATATGTTCAAAAAGATATTGTTGTTTCCATGATTAG 540

Qy 560 caagcaagtaatttctcccaagctgattttattcaatatgttacgttggtttaataaac 619  
Db 541 CAAGCAACTAATTTCTCCCAAGCTGATTTTATTCAATATGTTAGTGTGTTAATAAAC 600

Qy 620 ttttttagattta 633  
Db 601 TTTTATTAGATTTA 614

RESULT 2  
AA843663/c  
LOCUS  
DEFINITION  
ak08g10.s1 Soares\_parathyroid\_tumor\_NbHPA Homo sapiens cDNA clone  
IMAGE:1405410.3' similar to gb:J02874 FATTY ACID-BINDING PROTEIN,  
ADIPOCYTE (HUMAN);, mRNA sequence.

ACCESSION  
AA843663  
VERSION  
AA843663.1  
KEYWORDS  
EST.  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1. (bases 1 to 635)  
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Insert length: 681 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 472.  
Location/Qualifiers

FEATURES  
source

1. 635  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1405410"  
/clone\_lib="Soares\_parathyroid\_tumor\_NbHPA"  
/tissue\_type="parathyroid tumor"  
/dev\_stage="adult"  
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia  
) with a modified polylinker; Site.1: Not I; Site.2: Eco  
RI; 1st strand cDNA was primed with a Not I - oligo(dT)  
primer  
[5'-TGTTACCAATCTGAAGTGGAGCGCGGCACCAATTTTGTGTGTGTGTGTGT  
TTTTT-3'], double-stranded cDNA was size selected, ligated  
to Eco RI adapters (Pharmacia), digested with Not I and  
cloned into the Not I and Eco RI sites of a modified pT7T3  
vector (Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid  
adenomas was kindly provided by Dr. Stephen Marx, National  
Institute of Diabetes and Digestive and Kidney Diseases,  
NIH."

BASE COUNT 174 a 142 c 106 g 213 t  
ORIGIN

Query Match 94.9%; Score 601.4; DB 9; Length 635;  
Best Local Similarity 99.0%; Pred. No. 1.4e-151;  
Matches 605; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 16 tgcagcttccttccaccttgaaagaataatcctcagaaactcaaaaaatgtgtgatgctt 75  
Db 635 TGCAGCTTCCTCTCACCTTGAAGAATAATCTTGAAAACTCACAAGATGTGTGATGCTT 576

Qy 76 ttgtaggtacctggaacctgtctccagtgaaacctttgatgattatgaaagaagtag 135  
Db 575 TTGTAGGTACCTGGAAACTTGTCTCCAGTGAAACTTTTGATGATGATTTATGAAGAAGTAG 516

Qy 136 gagtgggcttggccaccaggaaagtggctggcatggcgccgcaaaccttaacatgatcatcagtg 195  
Db 515 GAGTTGGCTTTGCCACCAGGAAAGTGGCTGGCATGGCCAAACCTTAACATGATCATCAGTG 456

Qy 196 tgaatggggatgtgatccaccttaaatctgaaagtacacctttaaataactagatttcc 255  
Db 455 TGAATGGGGATGTGATCACCATTAAATCTGAAAGTACCTTTTAAAAATACTGAGATTTCT 396

Qy 256 tcatactggccagaaatttgaacaaagtcaactgcagatgcagaaagtcaagagaccca 315  
Db 395 TCATACTGGGCCAGGAATTTGACGAAGTCACTGCAGATGACGAAAGTCAAGGACACCA 336

Qy 316 taaccttagatgggggtgtcctgtgtacatgtgcgaaatggatgggaataacaacacca 375  
Db 335 TAACCTTAGATGGGGTGTCTCTGTACATGTGCAGAAATGGGATGGAATAACACACCA 276

Qy 376 taaagagaaaaacgagagatgataaactggtgtggaatgcgtcatgaaagcgctcactt 435  
Db 275 TAAAGAAAAACGAGAGATGATAAATCTGGTGGATGCTCATGAAGCGCTCACTT 216

Qy 436 ccacgagatttatgagagacataaaccaggaagcgttgacctggactgaagttcgat 495  
Db 215 CCACGAGATTATGAGAGACATAAGCCAAAGGACGTTGACCTGGACTGAAGTTGCGAT 156

Qy 496 tgaactacaacattctgtgggatatattgttccaaagaaagatattgttttccctgat 555  
 Db 155 TGAACCTTACAACATTTCTGGGATATTATTGTTCAAAAAGATATTGTTGTTTCCATGAT 96  
 Qy 556 ttagcaagcaagtaattttcccaagctgatatttattcaatatggttacgtggttaaa 615  
 Db 95 TTAGCAAGCAACTAATTTTCTCCCAAGCTGATTTTATTCATATGTTACGTTGGTTAAA 36  
 Qy 616 taactttttt 626  
 Db 35 TAAACTTTTT 25

RESULT 3  
 BG570228 636 bp mRNA linear EST 10-APR-2001  
 LOCUS 602590629F1 NIH\_MGC\_77 Homo sapiens cDNA clone IMAGE:4717518 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BG570228  
 VERSION BG570228.1 GI:13577881  
 KEYWORDS EST.  
 RCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 636)  
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: CLONTECH Laboratories, Inc.  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLCMI567 row: i column: 07  
 High quality sequence stop: 632.  
 Location/Qualifiers  
 1. .636  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4717518"  
 /clone\_lib="NIH\_MGC\_77"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site: 1:  
 Sfil (ggcgctcgcc); Site 2: Sfil (ggccattatgcc); 5' and  
 3' adaptors were used in cloning as follows: 5' adaptor  
 sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:  
 5'-ATTCTAGAGCCGAGCGCGCAGATG-dt(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size 1.9  
 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA). Note: this is a NIH\_MGC Library."

BASE COUNT 206 a 114 c 144 g 172 t  
 ORIGIN

Query Match 94.4%; Score 598.6; DB 10; Length 636;  
 Best Local Similarity 98.4%; Pred. No. 8.2e-151;  
 Matches 615; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

Qy 6 tccaggagggtgcagcttcttccacttgaagaataatcctagaaacctcacaagt 65  
 Db 10 TCCTGAACATGCGAGCTTCTCTACCTTGAAGAATAATCTGAAACATCACAAAATG 69  
 Qy 66 tgtgatctttttaggtacctggaactgtctccagtgaaactttgatgttatatg 125  
 Db 70 TGTGATGCTTTTGTAGTACCTGGAACACTGTCTCCAGTGAAACTTTGATGATATATG 129

Qy 126 aaagaagtagaggtgggttttccaccaggaaagtgtgctggcatggccaaacctaaacatg 185  
 Db 130 AAAGAAGTAGGAGTGGGCTTTTGCCACCAGGAAGTGGCTGGCATGGCCAAACCTAACATG 189  
 Qy 186 atcatcagtggaatggggtgtgattcaccattaaatgaaagtacattttaaataact 245  
 Db 190 ATCATCAGTGTGAATGGGATGTGATCACCATTAAATCTGAAAGTACCTTTTAAANACT 249  
 Qy 246 gagatttccttcatactgggcccaggaaatttgacaaagtcacatgcagatgcagagaaagtc 305  
 Db 250 GAGATTTCTTCTACTTGGGCCAGGAATTTGACGAAGTCACTGCAGATGACAGGAAAGTC 309  
 Qy 306 aagagcaccataaccttagatgggggtgtcctgtgatacatgtgcagaaatggggtggaata 365  
 Db 310 AAGAGCACCATAAACCCTTAGATGGGGGTCTCCTGTATACATGTGCAGAAATGGGATGGAATA 369  
 Qy 366 tcaaccaccataaagagaacacagagagatataaactggtggtggaatgcgtcatgaaa 425  
 Db 370 TCAACCACCATAAAGAGAAACAGAGAGATGATAAAGTGGTGGTGAATGCGTCATGAAA 429  
 Qy 426 gggtcacttcacgagaggtttatgagagagcataagccaaaggagcgttgacctggactg 485  
 Db 430 GGCCTCACTTCCACGAGAGTTTATGAGAGAGCATAAAGCCAAAGGACGTTGACCTGGACTG 489  
 Qy 486 aagttcattgaactcaacattctgtggatattgttccaaagatattgtt 545  
 Db 490 AAGTTCGATTGAACCTCTACAACTTCTGTGGATATATTGTTCAAAAAGATATGTTGT 549  
 Qy 546 ttccctgattagcaagcaagtaatttctcccaagctgattttattcaatatggttac 605  
 Db 550 TTTCATGATTTAGCAAGCAACTAATTTCTCCCAAGCTGATTTTATTC-ATATGGTTAC 608  
 Qy 606 gttggttaataacttttttagat 630  
 Db 609 GTTGGTTAAATAAATCTTTTATAGAT 633

RESULT 4  
 BG288820 632 bp mRNA linear EST 21-FEB-2001  
 LOCUS 602388151F1 NIH\_MGC\_93 Homo sapiens cDNA clone IMAGE:4516981 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BG288820  
 VERSION BG288820.1 GI:13044042  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 632)  
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLCMI0409 row: e column: 14  
 High quality sequence stop: 604.  
 Location/Qualifiers  
 1. .632  
 /organism="Homo sapiens"  
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 /clone="IMAGE:4516981"  
 /clone\_lib="NIH\_MGC\_93"  
 /tissue\_type="transitional cell papilloma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: bladder; Vector: pCMV-SPORT6; Site: 1: NotI;





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Qy 496 tgaactacacattctgtgggatataattgtccaaaaagatattgtgttttccctgat 555
Db 140 TCAACTCTACAACTATCTGTGGGATATATTGTTCAAAAAGATATGTTGTTTCCCATG 81
Qy 556 ttagcaagcaagtaattctcccaagctgatttattcaatatggttacctgtgtaaa 615
Db 80 TTAGCAAGCACTAATTTCTCCCAAGCTGATTTATTCAATATGTTTACGTTGGTTAAA 21
Qy 616 t-aacttttttagatttag 634
Db 20 TAAACTTTTTTAGATTAG 1

RESULT 6
BG434107 903 bp mRNA linear EST 14-MAR-2001
LOCUS 602506025F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4603278 5',
DEFINITION mRNA sequence.
ACCESSION BG434107
VERSION BG434107.1 GI:13340613
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 903)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Clontech Laboratories, Inc.
cDNA Library Preparation: Clontech Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM1337 row: a column: 07
High quality sequence stop: 624.
FEATURES
source
1. 903
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4603278"
/clone_lib="NIH_MGC_79"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: placenta; Vector: pDNR-LIB (Clontech);
Site 1: SfII (ggcgcctggcc); Site 2: SfII (ggcattatggcc
); 5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ATTCTAGAGCCGAGCGCCGACATG-dt(30)BN-3'
(sequence: 5'-ATTCTAGAGCCGAGCGCCGACATG-dt(30)BN-3'
(where B = A, C, G, or N = A, C, G, or T). Average
insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."
BASE COUNT 276 a 204 c 217 g 206 t
ORIGIN

Query Match 94.2%; Score 597.2; DB 10; Length 903;
Best Local Similarity 97.1%; Pred. No. 2.le-150;
Matches 608; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 6 tccagagggtgcagcttccttcacattgaagaataactctagaaactcacaaaaatg 65
Db 11 TCCGAAACGTCAGCTTCCTTCACCTTGAAGAATAATCTGAAACACACAAAATG 70
Qy 66 tgtgatgctttttaggtacacctggaacttctccagtgaaactttgatgattatg 125
Db 71 TGTGATGCTTTTGTAGGTACTGCGAAACTTCTCTCCAGTGAACACTTTGATGATTATG 130

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Qy 126 aagaagtaggagtggtgttggccaccaggaaagtggctgcatggccaaacctaacatg 185
Db 131 AAAGAAGTAGGAGTGGGCTTTGGCCACCAGGAAAGTGGCTGGCATGCCCAACCTAACATG 190
Qy 186 atcatcagtgaatggggatgtgataccatttaaatgaagtacatttaaaataact 245
Db 191 ATCATCAGTGAATGGGGATGTGATCACCATTAAATCTGAAGTACCTTTAAAAATACT 250
Qy 246 gagatttcttcatactggccaggaaatttgacgaagtcactgcagatgacaggaagtc 305
Db 251 GAGATTTCTTCACTGGCCAGGAATTGACGAAGTCACTGCAGATGACAGGAAGTC 310
Qy 306 aagagcaccataaccttagatgggggtgtcctgtgtacatgtgcagaatgggatgaaaa 365
Db 311 AAGAGCACCATAACCTTAGATGGGGGTGTCTGTGTACATGTGCAGAAATGGGATGAAAA 370
Qy 366 tcaaccaccataaagagaaaaacgagagatgataaactgggtggaatgcgtcatgaaa 425
Db 371 TCAACCACCATAAAGAGAAAACGAGAGATGATAAATCTGGGTGGATGCGTCATGAAA 430
Qy 426 ggcgtcacttccacgagagatttatgagagacataagccaaagggagcttgacctgga 485
Db 431 GCGTCACTTCCACGAGAGTATTATGAGAGAGCATTAAGCCAAAGGGACGTTGACCTG 490
Qy 486 aagttcgattgaactctacaacattctgtgggatataattgttcaaaagatatgttgt 545
Db 491 AAGTTCGCAATTGAACCTTACAAACATTCGTGGGATATATGTTCAACACAGATATTG 550
Qy 546 ttccctgatttagcaagcaagtaatttctcccaagctgatttattcaatatggttac 605
Db 551 TTTCCATGATTAGTACCAACACTAATTTCTCCCAAGCTGATTTTATCAATATGTTAC 610
Qy 606 gttggttaataaacttttttagatt 631
Db 611 GTTGCTTAATAAATCTTCTCTAGATT 636

RESULT 7
AI652163/3 630 bp mRNA linear EST 17-DEC-1999
LOCUS wb47g01.x1 NCI-CGAP GC6 Homo sapiens cDNA clone IMAGE:2308848 3',
DEFINITION similar to gb:J02874 FATTY ACID-BINDING PROTEIN, ADIPOCYTE (HUMAN
); mRNA sequence.
ACCESSION AI652163
VERSION AI652163.1 GI:4736142
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 630)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 717 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 404.
FEATURES
source
1. 630
/organism="Homo sapiens"

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/db_xref="taxon:9606"
/clone="IMAGE:230848"
/clone_lib="NCI_CGAP_GC6"
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/lab_host="DH10B"
/notes="Vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
from the normalized library NCI_CGAP_GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonedIDs
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
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BASE COUNT 171 a 142 c 106 g 210 t 1 others

ORIGIN

Query Match 94.1%; Score 596.4; DB 9; Length 630;  
Best Local Similarity 98.8%; Pred. No. 3.2e-150;  
Matches 600; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 20 gcttccttcacacttggaataatcctagaaaactcacaaaatgtgtgattgtt 79  
Db 630 GCTTCCTTTCACCTTGAAGATAATCTAGAAAACCTCACAAAAGGTGTGCTTTTGT 571  
Qy 80 aggtacctggaactgtctccagtgaaactttgatgattatgaagaagtagagt 139  
Db 570 AGGTACCTGGAACCTGTCTCCAGTGAACCTTTGATGATTATATGAAGAAGTAGGAGT 511  
Qy 140 ggggtttgccaccaggaaagtggctggcatggccaaacctcaacatgatcatcagtgtaa 199  
Db 510 GGGGCTTTGCCACCAGGAAGTGGCTGGCATGGCCAAACCTAACATGATCATCAGTGTGAA 451  
Qy 200 tgggagtgtatcaccataatgaatgaagtaacacctttaaaatactgagatttcctcat 259  
Db 450 TGGGGATGTATACCACTTAATACTGAAGTACCTTTTAAAAATACTGAGATTCTCTCAT 391  
Qy 260 actggccaggaaatttgacgaagtcactgcagatgacaggaagtcgaagcaccataac 319  
Db 390 ACTGGCCAGGAATTTGACGAAGTCACTGCAGATGACAGGAAGTCAAGACACCATTAAC 331  
Qy 320 cttagatgggggtgtcctgtgtacatgtgcagaaatggatggaaatacaaccacataaa 379  
Db 330 CTTAGATGGGGGTGTCTGTGTACATGTGCAGAAATGGGATGGAAATCACCCNCCATAAA 271  
Qy 380 gagaaacgagagataaactgaactggtgtgaatgcctcatgaaggcgtcacttccac 439  
Db 270 GAGAAACGAGAGGATGATAACCTGGTGGTGAATGCGTCAATGAAGGCGTCACTTCCAC 211  
Qy 440 gaggtttatgagagacataagcgaaggacgttgactggactgaagttcgcattgaa 499  
Db 210 GAGAGTTTATGAGAGACATAAGCAAGGACGTTGACCTGGAGTTCGCAATTGAA 151  
Qy 500 ctctacaactctgtgggtatattgttcaaaaagatatgttgttttccctgatttag 559  
Db 150 CTCTACACACTCTGTGGGATATATGTTCAAAAAGATATGTTGTTTCCATGATTAG 91  
Qy 560 caagcaagtaatttctcccaagctgattttattcaatatgtttacgttggttaataaac 619  
Db 90 CAAGCACTAATTTCTCCCAAGCTGATTTTATTCAATATGTTTACGTTGTTGTTAAATAA 31  
Qy 620 ttttttt 626  
Db 30 CTTTTTTT 24

RESULT 8  
AI651387/c  
LOCUS  
DEFINITION  
wb05f06.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:230848 3'  
similar to gb:J02874 FATTY ACID-BINDING PROTEIN, ADIPOCYTE (HUMAN  
).. mRNA sequence.

AI651387 GI:4735366  
EST.  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 635)  
NCI\_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Insert Length: 698 Std Error: 0.00  
Seq primer: -40up from Gibco  
High quality sequence stop: 470.  
Location/Qualifiers  
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/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/note="Vector: p7T3D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; Plasmid DNA  
from the normalized library NCI\_CGAP\_GC4 was prepared, and  
ss circles were made in vitro. Following HAP purification,  
this DNA was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from a pool  
of 5,000 clones made from the same library (clonedIDs  
1257096-1258631, 1469064-1470983, and 1475592-1476743).  
Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 174 a 146 c 107 g 206 t 2 others

ORIGIN

Query Match 94.0%; Score 596; DB 9; Length 635;  
Best Local Similarity 98.9%; Pred. No. 4.1e-150;  
Matches 610; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Qy 19 agcttccttcacacttggaataatcctagaaaactcacaaaatgtgtgattgtt 78  
Db 631 AGCTTCCTTTCACCTTGAAGATAATCTAGAAAACCTCCANAAATGTGTGATGCTTTTG 572  
Qy 79 tagtacctggaactgtctccagtgaaactttgtgatttatataaagaagtagag 138  
Db 571 TAGTACCTGGAACCTTGCTCTCCAGTGAAACTTTTGATGATTATATGAAGAAGTAGGAG 512  
Qy 139 tgggctttgccaccaggaaagtggctggcatggccaaacctcaacatgatcatcagtgta 198  
Db 511 TGGGCTTTGCCACCAGGAAGTGGCTGGCATGGCCAAACCTTAACATGATCATCATGTGTA 452  
Qy 199 atggggatgtatcaccattaaatcctgaaagtacatttaaaatactgagatttccttca 258  
Db 451 ATGGGGATGTGATCACCATTAAATCTGAAGTACCTTTAAAAAATCTGAGAGATTCCTTCA 392  
Qy 259 tactgggcccaggaatttgacgaagtcactgcagatgcagagaaagtcgaagcaccataa 318  
Db 391 TACTGGGCGCAGGAATTTGACGAAGTCACTGCAGATGACAGGAAAGTCAAGAGCACCATAA 332  
Qy 319 ccttagatgggggtgtcctgtgtacatgtgcagaaatggatgggaaatcaaccaccataa 378  
Db 319 ccttagatgggggtgtcctgtgtacatgtgcagaaatggatgggaaatcaaccaccataa 378

Db 331 CCTTAGATGGGGGTCTCTGTACATGTGCAGAAATGGGATGGAAATCAACCCCATAA 272  
Qy 379 agagaaacagagagatgataaaactggtggtggaatcgctcatgaaaggcctactcca 438  
Db 271 AGAGAAAACGAGAGATGATGAACCTGGTGGTGAATCGGTATGAAGGCGCTCACTTCCA 212  
Qy 439 cgagagttatgagagacataaagcgaagacgttgacctggaactgaagtcgattga 498  
Db 211 CGAGAGTTTATGAGAGAGCATAAACCAAGGACGTTGACCTGGGACTGAAGTTCGCAATGA 152  
Qy 499 acttacaacattctgtgggatattgttcaaaaagatatgttgttttccctgattta 558  
Db 151 ACTTACAACATCTGTGGGATATATTGTTCAAAAAGATATTGTTGTTTCCATGATTTA 92  
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Db 91 GCAAGCAACTAAATTTCTCCCAAGCTGATTTTATTAATATGTTACGTTGGTTAAATAA 32  
Qy 618 acttttttagatttag 634  
Db 31 ACTTTTTTAGATTAG 15

RESULT 9  
AL047557  
LOCUS AL047557 637 bp mRNA linear EST 01-MAR-2000  
DEFINITION DKFZ586E0221\_r1 586 (synonym: hutel) Homo sapiens cDNA clone  
ACCESSION DKFZ586E0221, mRNA sequence.  
VERSION AL047557  
KEYWORDS AL047557.3 GI:5936382  
SOURCE EST.  
ORGANISM human.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Ottewaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and  
Wiemann, S.  
EST (Ottewaelder, et al.)  
Unpublished (1999)  
On Apr 30, 1999 this sequence version replaced gi:5866815.  
Contact: Ottewaelder B  
MIPS  
Am Klopferspitz 18a D-82152 Martinsried, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by Medigenomix (Martinsried/Germany) within the cDNA  
sequencing consortium of the German Genome Project. s1 sequence  
also available  
This clone (DKFZ586E0221) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES  
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/organism="Homo sapiens"  
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/dev\_stage="adult"  
/lab\_host="DH10B"  
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BASE COUNT  
ORIGIN 214 a 106 c 146 g 171 t

Query Match 93.1%; Score 590.4; DB 9; Length 637;  
Best Local Similarity 98.9%; Pred. No. 1.3e-148;  
Matches 605; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Qy 16 tgcagcttccttcaccttgaagataatccttagaaaactcacaaaatgtgtgatgctt 75  
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Db 1 TGCAGCTTCCTTCTCACCTTTGAAGAAATAACTCTAGAAAACTCACAAAATGTGTGATGCTT 60  
Qy 76 ttgtaggtacgtgaaacttgtctccagtgaacttttgatgatttatatgaagaagttag 135  
Db 61 TTGTAGGTACCTGGAAACTTGTCTCCAGTGAACCTTTTGTATGATTATATGAAGAAGTAG 120  
Qy 136 gagtgggctttgccacacaggaagtggctgcatggcgaacacctaactaatcatcatg 195  
Db 121 GAGTGGGCTTTGCCACCAGGAAGTGGCTGGCATGGCCAAACCTAACATGATCATCAGTG 180  
Qy 196 tgaatgggagtgatcacaccattaaactgaaagtacacctttaaataactgagatttct 255  
Db 181 TGAATGGGGATGTGATCACCATTAACTCTGAAGTACCTTTAAAAAATACTGAGATTTCCT 240  
Qy 256 tcatactgggcccaggaatttgacgaagtcaactgcagatgcacaggaaagtcaagagacaca 315  
Db 241 TCATACTGGGCCAGGAATTTGACGAAGTCACTGCGAGATGACAGGAAAGTCAAGAGACCA 300  
Qy 316 taacctagatggggtgctcctggtacatgtgcagaatgggatggaatacaacacaca 375  
Db 301 TAACCTTAGATGGGGGTGCTCTGGTACATGTGCAGAAATGGGATGGAATAATCAACACCA 360  
Qy 376 taaagagaaaaacagagagatgataaaactgggtggtggaatgcgtcatgaaagcgtcactt 435  
Db 361 TAAAGAGAAAAACGAGAGGATGATAAACTGGTGGTGAATGCGTCATGAAAGCGTCACCT 420  
Qy 436 ccaagagagtttatgagagacataagccaaggcgcttgacctggaactgaagtcgat 495  
Db 421 CCACGAGAGTTTATGAGAGAGCATAAAGCCAAGGACGTTGACCTGGACTGAAGTTCCGAT 480  
Qy 496 tgaactctacaacattctgtgggatattgttcaaaaagatatgttgttttccctgat 555  
Db 481 TGAACCTACAACTATCTGTGGGATATATTGTCAAAAGATATTGGTGTTCATGAT 540  
Qy 556 tttagcaagcaagtaattttctcccaagctgattttattcaaat-gggtacgttggttaa 614  
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Qy 615 ataactttttt 626  
Db 601 ATAACTTTTTT 612

RESULT 10  
BG287253  
LOCUS BG287253 678 bp mRNA linear EST 21-FEB-2001  
DEFINITION 602381981P1 NIH\_MGC\_93 Homo sapiens cDNA clone IMAGE:4499252 5',  
mRNA sequence.  
ACCESSION BG287253  
VERSION BG287253.1 GI:13040909  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 678)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM10363 row: b column: 21  
High quality sequence stop: 625.  
Location/Qualifiers  
1..678  
/organism="Homo sapiens"

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

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/db_xref="taxon:9606"  
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Site_2: SalI; Cloned unidirectionally; oligo-dr primed.  
Average insert size 1.7 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH_MGC Library."
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BASE COUNT 225 a 130 c 152 g 171 t

Query Match 92.98; Score 588.8; DB 10; Length 678;  
Best Local Similarity 98.78; Pred. No. 3.6e-148;  
Matches 604; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

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19 TGCAGCTTCCTTCACCTTGAAGATAATCTCTAGAAACTCACAAAATGTGTGATGCTT 78  
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76 ttgtagtagtacctgaaactgtctccagtgaaactttgatgatttatataaagaagtag 135  
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79 TTGTAGGTACCTGGAAACTTGTCTCCAGTGAATACTTTGATGATTATATGAAGAAGTAG 138  
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136 gagtgggcttggcaccaggaagtggctggcatggccaaacctaaactgatcatcagtg 195  
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139 GAGTGGGCTTTGCCACGAGAAAGTGGCTGGCATGGCCAAACCTTAACATGATCATCAGTG 198  
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196 tgaatggggatgtgatcaccattaaatctgaagtacacttttaaaatactgagatttcc 255  
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199 TGAATGGGATGTGATCACCATTAAATCTGAAGTACCTTTAAAAATACTGAGATTTCCT 258  
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256 tcatactggccaggaatttgacaagtctactgcagatgacagaaagtcgaagaccaca 315  
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259 TCATACTGGGCCAGGAATTTGACGAAGTCACTGCAGATGACAGAAAGTCAAGACACCA 318  
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316 taaccttagatgggggtgtcctgtgtacatgtgcagaatggatggaaatcaaccacca 375  
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319 TAACCTTAGATGGGGTGTCTGTGTACATGTGCAGAAATGGGATGGAAATCAACCACCA 378  
|||||  
376 taaagaaacagagagatgataaactgtgtggaatgcgtcatgaaaggcgtcaactt 435  
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379 TAAAGAAACAGAGAGATGATAAATCTGTGTGGATGGTGCATGAAAGCGCTCACTT 438  
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436 ccagagagttatgagagacataagccaaggacgttgacctggactgaagtgcgat 495  
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439 CCAGAGAGTTTATGAGAGACATAAGCCAAGGACGTTGACCTGGACTGAAGTTCGCAT 498  
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496 tgaactctacaacttctgtgggatattgttcaaaaagatatgtgttttccctgat 555  
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499 TGAACCTACAACTTGTGGGATATATGTTCAAAAGATATCGTCGTTTCCATGAT 558  
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556 ttagaagcaagtaattttctccc-aagctgattttatccaatggttaoagttggttaa 614  
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559 TTAGCAAGCAACTAATTTCTCCCAAGAGCTGATTTTATCAATATGTTACGGTGGTTAA 618  
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615 ataactttttt 626  
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619 ATAACTTTT 630
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RESULT 11  
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LOCUS  
DEFINITION  
xnm71507.x1 NCI\_CGAP\_Kid11 Homo sapiens cDNA clone IMAGE:2689621 3'-  
similar to gb:J02874 FATTY ACID-BINDING PROTEIN, ADIPOCYTE (HUMAN  
); mRNA sequence.  
ACCESSION  
AW237388  
VERSION  
AW237388.1 GI:6569777  
KEYWORDS  
EST.  
human.  
SOURCE

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS  
TITLE  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL  
COMMENT  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Seq primer: -40UP from Gibco  
High quality sequence stop: 450.  
FEATURES  
Location/Qualifiers  
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Plasmid DNA from the normalized library NCI\_CGAP\_Kid3 was  
prepared, and ss circles were made in vitro. Following HAP  
purification, this DNA was used as tracer in a subtractive  
hybridization reaction. The driver was PCR-amplified cDNAs  
from a pool of 5,000 clones made from the same library  
(cloneIDs 1323376-1323911, 1456007-1456775, and  
1500552-1502855). Subtraction by Bento Soares and M.  
Fatima Bonaldo."

BASE COUNT 172 a 141 c 106 g 197 t

Query Match 92.48; Score 586; DB 9; Length 616;  
Best Local Similarity 99.08; Pred. No. 2e-147;  
Matches 600; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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Qy 81 ggtacctggaaactgtctccagtgaatactttgatgattatgaaagaagtaggagtg 140  
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Db 553 GGTACCTGGAACCTGTCTCCAGTGAACACTTTTGATGATTATATGAAAGAGTAGAGTG 494  
|||||  
Qy 141 ggccttgcaccaggaagtgctggcatggccaaacctcaatcatcatcagtgtaagt 200  
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Db 493 GCGTTTGCACACAGAAAGTGGCTGGCATGGCCAAACCTTAACATGATCATCAGTGAAT 434  
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Qy 201 ggggatgtgacacattcaatctgaaagtacacctttaaatactgagatttccctcata 260  
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Db 433 GGGGATGTGATCACCATTAAATCTGAAAGTACCTTTAAATACTGAGATTTCCCTCAT 374  
|||||  
Qy 261 ctgggcccagggaatttgacgaagtcactgcagatgacagggaagtcgaagagcaccataacc 320  
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Db 373 CTGGGCCAGGAATTTGACGAAGTCACTGCAGATGACAGGAAGTCAAGAGCACCATAACC 314  
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Qy 321 ttagatgggggtgctcctgggtacatgtgcagaaatgggagtgaaataaccaccataaag 380  
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Qy 501 tctcaacattctgtgggatatattgtccaaaagataattgttttccctgatttagc 560
Db 133 TCTCAACATTCTGTGGGATATATGTTCAAAAGATATGTTGTTTCCATGATTAGC 74
Qy 561 aagcaagtaatttctcccaagctgattttcaataatggttacgttggttgaataact 620
Db 73 AAGCAACTAATTTCTCCCAAGCTGATTTTATCAATATGTTAGCTGGTTAAATAAAC 14
Qy 621 tttttt 626
Db 13 TTTTTT 8

RESULT 12
LOCUS BG261014 900 bp mRNA linear EST 13-FEB-2001
DEFINITION 602372632F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4480759 5',
mRNA sequence.
ACCESSION BG261014
VERSION BG261014.1 GI:12770830
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 900)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10314 row: p column: 08
High quality sequence start: 2
High quality sequence stop: 625.
Location/Qualifiers
1. 900
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Average insert size 1.7 kb. Library enriched for
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Note: this is a NIH_MGC Library."

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Best Local Similarity 98.5%; Pred. No. 4.le-147;
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Qy 136 gagtgggttttgcaccaggaaagtgggtggcattgcccacacccatgatcatcagtg 195
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DEFINITION 602381388F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4499181 5',
mRNA sequence.
ACCESSION BG289969
VERSION BG289969.1 GI:13046293
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 632)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10362 row: o column: 22
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FEATURES
source

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ACCESSION BG287532  
VERSION BG287532.1 GI:13041458  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 654)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
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Site\_2: SalI; Cloned unidirectionally; oligo-dT primed.  
Average insert size 1.7 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: This is a NIH\_MGC Library."  
218 a 115 c 149 g 171 t 1 others

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Best Local Similarity 99.2%; Pred. No. 1.5e-146;  
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Db 127 GAGTGGGCTTTGGCCACGAGAAAGTGGCTGGCATGGCCAAAACCTTAACATCATCATCAGTG 186  
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Db 427 CCACGAGAGTTTATGAGAGAGCATAAAGCAAGGACGTTGACCTGGACTGAAGTTCCGAT 486  
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Db 546 TTAGCAAGCAACTAAATTTCTCCCAAGCTGATTTTATTCAATATGTTACGTTGGTTAAA 605  
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Total number of hits satisfying chosen parameters: 767066

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	63.6	10.0	7218	1	US-08-232-463-14
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7	50.2	7.9	924	2	US-08-241-664B-1
8	50.2	7.9	924	5	PCT-US93-03936-1
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	33	31.8	5.0	3930	3	US-09-162-373-2	Sequence 2, Appli
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	45	30.8	4.9	2074	3	US-09-248-137-11	Sequence 11, Appli

ALIGNMENTS

RESULT 1  
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; Sequence 3, Application US/08446600A  
; Patent No. 5719126  
; GENERAL INFORMATION:  
; APPLICANT: No. 5719126dlund, James J. and Farooqui, Jamal Z.  
; TITLE OF INVENTION: MELANOGENIC INHIBITOR, AND METHODS OF PRODUCING AND USING T  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Frost & Jacobs  
; STREET: 2500 PNC Center, 201 East Fifth St.  
; CITY: Cincinnati  
; STATE: OH  
; COUNTRY: USA  
; ZIP: 45202-4182  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446.600A  
; FILING DATE: 24 May 1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/980.513  
; FILING DATE: 24 No. 5719126ember 1992  
; APPLICATION NUMBER: PCT/US93/11139  
; FILING DATE: 16 No. 5719126ember 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ann G. Robinson  
; REGISTRATION NUMBER: 39,820  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (513) 651-6128  
; TELEFAX: (513) 651-6981  
; TELEX: 21-4396 F&J Gin  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 408 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Unknown  
; US-08-446-600A-3

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Best Local Similarity 62.7%; Pred. No. 1.9e-39;  
Matches 242; Conservative 0; Mismatches 144; Indels 0; Gaps 0;





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; LENGTH: 640 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: THIRNOT02  
; CLONE: 879706  
US-08-847-724-2

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## RESULT 6

US-08-468-709B-1  
; Sequence 1, Application US/08468709B  
; Patent No. 5654137  
; GENERAL INFORMATION:  
; APPLICANT: Astrom, Anders  
; APPLICANT: Voorhees, John  
; APPLICANT: Pettersson, Ulrika  
; APPLICANT: Cromie, Matthew  
; APPLICANT: Tavakkol, Amir  
; TITLE OF INVENTION: HUMAN CRABP-I AND CRABP-II  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.  
; STREET: PO Box 828  
; CITY: Bloomfield Hills  
; STATE: Michigan  
; COUNTRY: United States of America  
; ZIP: 48303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468,709B  
; FILING DATE: 06/06/95  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, Deann F.  
; REGISTRATION NUMBER: 36,683  
; REFERENCE/DOCKET NUMBER: 2115-00676DVF  
; TELEPHONE: (810) 641-1600  
; TELEFAX: (810) 641-0270  
; TELEX: 287637  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 924 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA

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; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapien  
; TISSUE TYPE: skin  
; CELL TYPE: fibroblast  
; IMMEDIATE SOURCE:  
; LIBRARY: HUMAN SKIN FIBROBLAST LAMBDA GT11  
; CLONE: LAMBDA F1.1  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 99..515  
; OTHER INFORMATION: /codon\_start= 99  
; OTHER INFORMATION: /citation= ({1})  
; FEATURE:  
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; OTHER INFORMATION: /citation= ({1})  
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; NAME/KEY: 3'UTR  
; LOCATION: 516..924  
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; FEATURE:  
; NAME/KEY: polyA\_signal  
; LOCATION: 911..916  
; OTHER INFORMATION: /citation= ({1})  
; FEATURE:  
; NAME/KEY: terminator  
; LOCATION: 513..515  
; OTHER INFORMATION: /citation= ({1})  
; PUBLICATION INFORMATION:  
; AUTHORS: Astrom, Anders  
; AUTHORS: Tavakkol, Amir  
; AUTHORS: Pettersson, Ulrika  
; AUTHORS: Cromie, Matthew  
; AUTHORS: Elder, James T.  
; AUTHORS: Voorhees, John J.  
; TITLE: Molecular Cloning of Two Human Cellular  
; TITLE: Retinoic Acid-Proteins (CRABP)  
; JOURNAL: J. Biol. Chem.  
; DATE: 1991  
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 924  
; PUBLICATION INFORMATION:  
; AUTHORS: Astrom, Anders  
; AUTHORS: Tavakkol, Amir  
; AUTHORS: Elder, James T.  
; AUTHORS: Pettersson, Ulrika  
; AUTHORS: Cromie, Matthew  
; AUTHORS: Voorhees, John J.  
; TITLE: Cloning of CRABP II cDNA from Human Skin.  
; TITLE: Retinoic Acid Induces Expression of CRABP II but  
; TITLE: No. 5654137 CRABP in Human Skin in Vivo and in Dermal but  
; TITLE: No. 5654137 Lung Fibroblasts in Vitro  
; JOURNAL: J. Invest. Dermatol.  
; VOLUME: 96  
; PAGES: 547-547  
; DATE: April-1991  
US-08-468-709B-1

Query Match 7.9%; Score 50.2; DB 1; Length 924;  
Best Local Similarity 54.0%; Pred. No. 3.5e-06;  
Matches 128; Conservative 0; Mismatches 103; Indels 6; Gaps 1;

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Db 174 AATGTCATGCTGGAGGAGATTGCTGTGGCTGCAGCGTCCAGCCACCGACCTGGAGATCAAA 233  
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Db 294 TTCAAGGTTGGGAGGAGTTTGAGGAGCAGACTGTGGTGGGAGGCCCTGTAAGAGC 350

## RESULT 7

US-08-241-664B-1  
; Sequence 1, Application US/08241664B  
; Patent No. 5871909  
; GENERAL INFORMATION:  
; APPLICANT: Voorhees, John J.  
; APPLICANT: Astrom, Anders  
; APPLICANT: Patterson, Ulrika  
; APPLICANT: Tavakkol, Amir  
; TITLE OF INVENTION: HUMAN CRABP-I AND CRABP-II  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.  
; STREET: PO Box 828  
; CITY: Bloomfield Hills  
; STATE: Michigan  
; COUNTRY: United States of America  
; ZIP: 48303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/241,664B  
; FILING DATE: May 11, 1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, Deann F.  
; REGISTRATION NUMBER: 36,683  
; REFERENCE/DOCKET NUMBER: 2115-00676COD  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (810) 641-1600  
; TELEFAX: (810) 641-0270  
; TELEX: 287637  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 924 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapien  
; TISSUE TYPE: skin  
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; PUBLICATION INFORMATION:  
; AUTHORS: Astrom, Anders  
; AUTHORS: Tavakkol, Amir  
; AUTHORS: Pettersson, Ulrika  
; AUTHORS: Cromie, Matthew  
; AUTHORS: Voorhees, John J.  
; TITLE: Molecular Cloning of Two Human Cellular  
; TITLE: Retinoic Acid-Proteins (CRABP)  
; JOURNAL: J. Biol. Chem.  
; DATE: 1991  
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 924  
; PUBLICATION INFORMATION:  
; AUTHORS: Astrom, Anders  
; AUTHORS: Tavakkol, Amir  
; AUTHORS: Elder, James T.  
; AUTHORS: Pettersson, Ulrika  
; AUTHORS: Cromie, Matthew  
; AUTHORS: Voorhees, John J.  
; TITLE: Cloning of CRABP II cDNA from Human Skin:  
; TITLE: Retinoic Acid Induces Expression of CRABP II but  
; TITLE: No. 5871909 CRABP I in Human Skin in Vivo and in Dermal but  
; TITLE: No. 5871909 Lung Fibroblasts in Vitro  
; JOURNAL: J. Invest. Dermatol.  
; VOLUME: 96  
; PAGES: 547-547  
; DATE: April-1991  
; US-08-241-664B-1

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; GENERAL INFORMATION:  
; APPLICANT: Voorhees, John J.  
; APPLICANT: Astrom, Anders  
; APPLICANT: Patterson, Ulrika

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; AUTHORS: Elder, James T.
; AUTHORS: Voorhees, John J.
; TITLE: Molecular Cloning of Two Human Cellular
; TITLE: Retinoic Acid-Proteins (CRABP)
; JOURNAL: J. Biol. Chem.
; DATE: 1991
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 924
; PUBLICATION INFORMATION:
; AUTHORS: Astrom, Anders
; AUTHORS: Tavakkol, Amir
; AUTHORS: Elder, James T.
; AUTHORS: Pettersson, Ulrika
; AUTHORS: Cromie, Matthew
; AUTHORS: Voorhees, John J.
; TITLE: Cloning of CRABPII cDNA from Human Skin:
; TITLE: Retinoic Acid Induces Expression of CRABPII but
; TITLE: Not CRABI in Human Skin in Vivo and in Dermal but
; TITLE: Not Lung Fibroblasts in Vitro
; JOURNAL: J. Invest. Dermatol.
; VOLUME: 96
; PAGES: 547-547
; DATE: April-1991
; PCT-US93-03936-1

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; GENERAL INFORMATION:
; APPLICANT: Astrom, Anders
; APPLICANT: Voorhees, John
; APPLICANT: Pettersson, Ulrika
; APPLICANT: Tavakkol, Amir
; TITLE OF INVENTION: HUMAN CRABP-I AND CRABP-II
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESS: Harness, Dickey & Pierce, P.L.C.
; STREET: PO Box 828
; CITY: Bloomfield Hills
; STATE: Michigan
; COUNTRY: United States of America
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,709B
; FILING DATE: 06/06/95
; CLASSIFICATION: 435

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ATTORNEY/AGENT INFORMATION:  
NAME: Smith, Deann F.  
REGISTRATION NUMBER: 36,683  
REFERENCE/DOCKET NUMBER: 2115-00676DVF  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (810) 641-1600  
TELEFAX: (810) 641-0270  
TELEX: 287637  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 525 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo Sapien  
TISSUE TYPE: skin  
CELL TYPE: fibroblast  
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PUBLICATION INFORMATION:  
AUTHORS: Astrom, Anders  
AUTHORS: Tavakkol, Amir  
AUTHORS: Petterson, Ulrika  
AUTHORS: Cromie, Matthew  
AUTHORS: Elder, James T.  
AUTHORS: Voorhees, John J.  
TITLE: Molecular Cloning of Two Human Cellular  
TITLE: Retinoic Acid-Proteins (CRABP)  
JOURNAL: J. Biol. Chem.  
DATE: 1991  
RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 1 TO 525  
PUBLICATION INFORMATION:  
AUTHORS: Astrom, Anders  
AUTHORS: Tavakkol, Amir  
AUTHORS: Elder, James T.  
AUTHORS: Petterson, Ulrika  
AUTHORS: Cromie, Matthew  
AUTHORS: Voorhees, John J.  
TITLE: Cloning of CRABP II cDNA from Human Skin:  
TITLE: Retinoic Acid Induces Expression of CRABP II but  
TITLE: No. 5654137 CRABP in Human Skin in Vivo and in Dermal but  
TITLE: No. 5654137 Lung Fibroblasts in Vitro  
JOURNAL: J. Invest. Dermatol.  
VOLUME: 96  
PAGES: 547-547  
DATE: April-1991  
US-08-468-709B-3

Query Match 7.7%; Score 48.8; DB 1; Length 525;  
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; Sequence.3, Application US/08241664B  
; Patent No. 5871909  
; GENERAL INFORMATION:  
; APPLICANT: Voorhees, John J.  
; APPLICANT: Astrom, Anders  
; APPLICANT: Patterson, Ulrika  
; APPLICANT: Tavakkol, Amir  
; TITLE OF INVENTION: HUMAN CRABP-I AND CRABP-II  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.  
; STREET: PO Box 828  
; CITY: Bloomfield Hills  
; STATE: Michigan  
; COUNTRY: United States of America  
; ZIP: 48303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/241,664B  
; FILING DATE: May 11, 1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, Deann F.  
; REGISTRATION NUMBER: 36,683  
; REFERENCE/DOCKET NUMBER: 2115-00676COD  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (810) 641-1600  
; TELEFAX: (810) 641-0270  
; TELEX: 287637  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 525 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo Sapien  
; TISSUE TYPE: skin  
; CELL TYPE: fibroblast  
; IMMEDIATE SOURCE:  
; LIBRARY: human skin Lambda ZapII









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Copyright (c) 1993 - 2000 CompuGen Ltd.

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# SUMMARIES

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5	376.8	59.4	604	22 AAH34528	Human colon cancer
6	360	56.8	435	16 AAH21621	Human gene signatu
7	341.4	53.8	399	20 AAX32483	Porcine adipocyte
8	247.6	39.1	351	21 AAA37715	Mouse AFABP cDNA f
9	211.4	33.3	411	19 AAV10405	Human myelin P2 pr

10	205	32.3	276	21	AAZ42917	Human 5' EST isola
11	203	32.0	374	21	AAC86453	Mouse Ng-119K123 g
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14	159.4	25.1	8144	20	AAX32482	Porcine adipocyte
15	157.8	24.9	313	21	AAC86452	Mouse adipocyte li
16	155.8	24.6	662	22	AAS13247	Human DNA encoding
17	155.8	24.6	720	20	AAZ77538	Human ovarian tumo
18	155.8	24.6	1072	24	AAS94888	Human DNA sequence
19	155.6	24.5	408	15	AAQ66842	Melanogenic inhibi
20	143.2	22.6	613	19	AAQ68587	Nucleotide sequenc
21	143.2	22.6	731	18	AAZ74751	Human cytochrome I
22	143.2	22.6	731	19	AAV68225	Nucleotide sequenc
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37	71.4	11.3	550	23	AAS15722	DNA encoding fatty
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KW serum cholesterol; therapy; human; ss.  
OS Homo sapiens.  
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PE 11-FEB-2000; 2000WO-US03560.  
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PR 12-FEB-1999; 99US-0119880.  
XX (HARD ) HARVARD COLLEGE.  
XX Lee M, Perrella MA, Hotamisligil GS;



XX WIPI; 2000-506094/45.  
DR P-PSDB; AAY90320.  
XX  
PT Reducing expression of adipocyte fatty acid binding protein through  
PT administration of a compound is used to inhibit formation of an  
PT atherosclerotic lesion -  
XX  
PS Disclosure; Page 10; 43pp; English.  
XX  
CC This sequence represents the human AFABP (adipocyte fatty  
CC acid binding protein) cDNA sequence. The invention relates to a method  
CC for inhibiting formation of an atherosclerotic lesion comprising  
CC administering to a mammal a compound that reduces expression of adipocyte  
CC fatty acid binding protein (AFABP). The method is used to inhibit  
CC formation of atherosclerotic lesions. The method is used to identify  
CC compounds which can be used to inhibit formation of atherosclerotic  
CC lesions through inhibition of AFABP binding to an intracellular ligand  
CC in a macrophage or adipocyte, inhibition of development of an  
CC atherosclerotic lesion, inhibition of a macrophage differentiating into  
CC a foam cell or inhibition of AFABP expression in a cell. AFABP activity  
CC may be inhibited to treat atherosclerosis or to treat individuals at risk  
CC of developing atherosclerosis. Inhibiting AFABP expression or activity  
CC reduces the development of atherosclerotic lesions despite a high level  
CC of serum cholesterol.  
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Query Match 100.0%; Score 634; DB 21; Length 634;  
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KW antidiabetic; neuroprotective; antiviral; antiallergic; hepatotropic;  
KW antibacterial; antifungal; antiparasitic; cardiant; anticonvulsant;  
KW Addison's disease; allergy; autoimmune haemolytic anaemia;  
KW autoimmune thyroiditis; rheumatoid arthritis; Crohn's disease;  
KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;  
KW cardiovascular disorder; wound healing; neurological disease; ds.  
XX OS Homo sapiens.  
XX PN WO200055173-A1.  
XX PD 21-SEP-2000.  
XX PF 08-MAR-2000; 2000WO-US05881.  
XX PR 12-MAR-1999; 99US-0124270.  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX PI Rosen CA, Ruben SM;  
XX DR WPI; 2000-611515/58.  
XX PS P-PSDB; AAB58740.  
XX PT New human breast and ovarian cancer associated gene sequences and the  
PT polypeptides encoded by these genes, useful in the prevention,  
PT treatment and diagnosis of cancer, immune disorders, cardiovascular  
PT disorders and neurological diseases -  
XX Claim 1; Page 504; 1299pp; English.  
XX Sequences AAF21614 - AAF22031 represent DNA sequences encoding human  
CC proteins AAB58711 - AAB59128. The DNA and protein sequences are  
CC associated with breast and ovarian cancer. Included in the invention are  
CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the  
CC isolation and characterisation of the DNA and protein sequences of the  
CC invention. The breast and ovarian cancer associated DNA, protein, agonist  
CC or antagonist sequences exhibit cytostatic; immunosuppressive;  
CC neuroprotective; antiviral; antiallergic; hepatotropic;  
CC antidiabetic; antiinflammatory; antiparasitic and cardiant activity. The  
CC polynucleotide and protein sequences are used in the diagnosis of cancer,  
CC particularly breast and ovarian cancer. The nucleic acid sequences,  
CC proteins, agonists and antagonists may also be used in the diagnosis,  
CC prevention and treatment of immune disorders e.g. Addison's disease,  
CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,  
CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid  
CC arthritis and ulcerative colitis; cardiovascular disorders such as  
CC myocardial ischaemia; wound healing; neurological diseases such as  
CC cerebral anoxia and epilepsy; and infectious diseases.  
XX Sequence 709 BP; 227 A; 130 C; 167 G; 182 T; 3 other;

Query Match 93.8%; Score 594.6; DB 21; Length 709;  
Best Local Similarity 98.4%; Pred. No. 7.2e-168;

Matches 611; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

Qy 6 tccaggagggtgcagcttctctccaccttgaaagaataatcctagaagaactcacaaaatg 65  
| | | | |  
Db 24 tccggaactgcagcttctctccaccttgaaagaataatcctagaagaactcacaaaatg 83  
| | | | |  
Qy 66 tgtgatgctttgttaggtacctggaaaacttgtctccagtgaaaactttgatgattatg 125  
| | | | |  
Db 84 tgtgatgctttgttaggtacctggaaaacttgtctccagtgaaaactttgatgattatg 143  
| | | | |  
Qy 126 aaagaagtaggagtggtttgcccaccaggaaaagtgctggcattgcccacaccttaacatg 185  
| | | | |  
Db 144 aaagaagtaggagtggtttgcccaccaggaaaagtgctggcattgcccacaccttaacatg 203  
| | | | |  
Qy 186 atcatcagtgaaatggggatgtgatcaccattaaatctgaaagtacatttaaaaatact 245  
| | | | |  
Db 204 atcatcagtgaaatggggatgtgatcaccattaaatctgaaagtacatttaaaaatact 263  
| | | | |  
Qy 246 gagatttcttcaactgggcaggaaatttgacgaagtcactgcagatgcagaggaaagtc 305  
| | | | |  
Db 264 gagatttcttcaactgggcaggaaatttgacgaagtcactgcagatgcagaggaaagtc 322  
| | | | |  
Qy 306 aagagcaccataaaccttagatgggggtgctcctgtacatgtgcagaaaatgggatggaaaa 365  
| | | | |  
Db 323 aagagcaccataaaccttagatgggggtgctcctgtacatgtgcagaaaatgggatggaaaa 382  
| | | | |  
Qy 366 tcaaccaccataaagagaaaacgagagatgataaaactggtgtggaatgcgtcatgaaa 425  
| | | | |  
Db 383 tcaaccaccataaagagaaaacgagagatgataaaactggtgtggaatgcgtcatgaaa 442  
| | | | |  
Qy 426 ggcgtcactccacgagatttatgagagagcataagccaaggagcgttgacctggactg 485  
| | | | |  
Db 443 ggcgtcactccacgagatttatgagagagcataagccaaggagcgttgacctggactg 502  
| | | | |  
Qy 486 aagttcgcatgaaactcacacattctgtgggatatattgttcaaaaagatatgttgt 545  
| | | | |  
Db 503 aagttcgcatgaaactcacacattctgtgggatatattgttcaaaaagatatgttgt 562  
| | | | |  
Qy 546 ttccctgatttagaagaagaatatttctcccaagctgattttattcaaatatgtgttac 605  
| | | | |  
Db 563 ttccctgatttagaagaagaatatttctcccaagctgattttattcaaatatgtgttac 622  
| | | | |  
Qy 606 gttgtttaaataaactttttt 626  
| | | | |  
Db 623 gttgggttaaataaactttttt 643  
| | | | |

RESULT 3  
AAC10273  
AAC10273 standard; cDNA; 463 BP.

AC AAC10273;  
XX  
DT 06-OCT-2000 (first entry)  
XX  
DE Human secreted protein 5' EST, SEQ ID NO: 14348.  
XX  
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
KW gene therapy; chromosome mapping; ss.  
XX Homo sapiens.  
XX EP1033401-A2.  
PN  
PD 06-SEP-2000.  
XX  
PF 21-FEB-2000; 2000EP-0200610.  
XX  
PR 26-FEB-1999; 99US-0122487.  
XX (GEST ) GENSET.  
XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.  
DR  
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
XX  
PS Claim 1; SEQ ID 14348; 71pp + CD-ROM; English.  
XX  
CC The present sequence is one of a large number of 5' ESTs derived from  
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively  
CC identified within the present sequence. The 5' ESTs were prepared from  
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST  
CC sequences usually correspond mainly to the 3' untranslated region (UTR)  
CC of the mRNA because they are often obtained from oligo-dT primed cDNA  
CC libraries. Such ESTs are not well suited for isolating cDNA sequences  
CC derived from the 5' ends of mRNAs and even in those cases where longer  
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.  
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be  
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used  
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.  
CC They are used to obtain upstream regulatory sequences and to design  
CC expression and secretion vectors.  
XX  
SQ Sequence 463 BP; 154 A; 87 C; 113 G; 108 T; 1 other;

Query Match 68.2%; Score 432.6; DB 21; Length 463;  
Best Local Similarity 98.5%; Pred. No. 1.9e-119;  
Matches 446; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

Qy 6 tccaggagggtgcagcttctctccaccttgaaagaataatcctagaagaactcacaaaatg 65  
| | | | |  
Db 12 tctgaaaactgcagcttctctccaccttgaaagaataatcctagaagaactcacaaaatg 71  
| | | | |  
Qy 66 tgtgatgctttgttaggtacctggaaaacttctccagtgaaaactttgatgattatg 125  
| | | | |  
Db 72 tgtgatgctttgttaggtacctggaaaacttctccagtgaaaactttgatgattatg 131  
| | | | |  
Qy 126 aaagaagtaggagtggtttgcccaccaggaaaagtgctggcattgcccacaccttaacatg 185  
| | | | |  
Db 132 aaagaagtaggagtggtttgcccaccaggaaaagtgctggcattgcccacaccttaacatg 191  
| | | | |  
Qy 186 atcatcagtgaaatggggatgtgatcaccattaaatctgaaagtacatttaaaaatact 245  
| | | | |  
Db 192 atcatcagtgaaatggggatgtgatcaccattaaatctgaaagtacatttaaaaatact 251  
| | | | |  
Qy 246 gagatttcttcaactgggcaggaaatttgacgaagtcactgcagatgcagaggaaagtc 305  
| | | | |  
Db 252 gagatttcttcaactgggcaggaaatttgacgaagtcactgcagatgcagaggaaagtc 310  
| | | | |  
Qy 306 aagagcaccataaaccttagatgggggtgtcctgggtacatgtgcagaaaatgggatggaaaa 365  
| | | | |  
Db 311 aagagcaccataaaccttagatgggggtgtcctgggtacatgtgcagaaaatgggatggaaaa 370  
| | | | |  
Qy 366 tcaaccaccataaagagaaaacgagagatgataaaactggtgtggaatgcgtcatgaaa 425  
| | | | |  
Db 371 tcaaccaccataaagagaaaacgagagatgataaaactggtgtggaatgcgtcatgaaa 430  
| | | | |  
Qy 426 ggcgtcactccacgagattttatgagagagca 458  
| | | | |  
Db 431 ggcgtcactccacgagattttatgagagagca 463  
| | | | |

RESULT 4  
AAA37716  
ID AAA37716 standard; cDNA; 614 BP.  
XX  
AC AAA37716;  
XX  
DT 22-NOV-2000 (first entry)  
XX  
DE Mouse AFABP cDNA sequence.



CC inactive proteins or to supplement the patients own production of P.  
CC Additionally, N may be used to produce the colon cancer-associated Ps,  
CC by inserting the nucleic acids into a host cell and culturing the cell  
CC to express the proteins. N and P can be used in the prevention, diagnosis  
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204  
CC and AAB77789 represent sequences used in the exemplification of the  
CC present invention.  
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were  
CC missing at time of publication, meaning no sequences are present for  
CC SEQ ID NO:1027 to 1052, 7921 and 7922.  
XX  
XX Sequence 604 BP: 208 A; 115 C; 147 G; 134 T; 0 other:  
SQ

[illegible]

RESULT 6  
T21621  
AAT21621 standard; CDNA to mRNA: 435 BP.

AA	
AC	AAT21621;
XX	
DT	04-AUG-1996 (first entry)

24		
DE		
XX		
KW	Human gene signature HUMGS03056.	
KW	Gene signature; messenger RNA; mRNA; relative abundance; frequency;	
KW	human; cloning; mapping; non-biased library; diagnosis; detection;	
KW	cell typing; abnormal cell function; ss.	

XX Homo sapiens.  
OS  
XX  
PN WO9514772-A1.

XX	01-JUN-1995.	
PD		
XX		
PF	11-NOV-1994:	94WO-JP01916.

12-NOV-1993; 93JJP-  
(MATS/) MATSUBARA K.  
(OKUB/) OKUBO K.

XX	Matsubara K, Okubo K;
PI	
XX	WPI; 1995-206931/27.
XX	
DR	Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT	for diagnosis of abnormal cell function, by preparing cDNA that
PT	reflects relative abundance of corresp. mRNA in specific human
PT	tissues
PT	
XX	Claim 1; Page 925; 2245pp; Japanese.
XX	
CC	A single-stranded DNA (or its complementary strand or the corresp.
CC	double-stranded DNA) which comprises one of the 7837 "GS" sequences
CC	given in AAT19001-T26837 and which is able to hybridise to part of
CC	human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
CC	sequences were obtained from 3'-directed cDNA libraries prepared
CC	from various human tissues; synthesis of cDNA was initiated from the
CC	3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
CC	untranslated sequence is unique to a particular mRNA species, almost
CC	all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC	is constructed so as to reflect accurately the relative abundance of
CC	different mRNAs in the particular tissue from which it was derived.
CC	The appearance frequency of a given GS in a cDNA library can be
CC	determined (esp. using primers and probes derived from the GS
CC	sequences) as a means of diagnosing abnormal cell function or for
CC	recognising different cell types.
XX	
SO	Sequence 435 BP; 135 A; 68 C; 94 G; 117 T; 21 other;

Query Match	56.8%	Score 360;	DB 16;	Length 435;
Best Local Similarity	92.4%	Pred. No. 1e-97;		
Matches 389;	Conservative	0;	Mismatches 29;	Indels 3;
Gaps				

[illegible]

Qy	389	agaggatgataaactgggtggaagcgtcatgaaaggcgtcaacttccacgagagtta	448
Db	181	agagngtgataaactgggtggaagcgtcatgaaaggcgtcaacttccacgagagtta	240
Qy	449	tgagagagcataagccaaggagcgttgacctggactggaagttcgcatgaaactctcaac	508
Db	241	tgagagagcataagccaaggagcgttgacctggactggaagttcgcatgaaactctcaac	300
Qy	509	attctgtgggatatattgtttcaaaaagatatgtgtgttttccct-gatttagcaagcaag	567
Db	301	attntgtggngtatattgtttcaaaaagntatgtngttttcccatgatttagcaagcaac	360
Qy	568	taattttctcccaagcgtgattttatt--caatatgtgtacgttgggttaataacttttt	625
Db	361	taattttntcccaagcgtngnttttttttccaatantggttnacgttggntcaataaanntttt	420
Qy	626	t	626
Db	421	t	421

RESULT 7  
AAx32483  
ID AAX32483 standard; DNA; 399 BP.  
XX  
AC AAX32483;

[illegible]

```

Db 62 ggaacctggaagctgtctccagtgaaacacttcgatgattacatgaaagaagtgggagtg 121
Qy 141 ggctttgccaccaggaagtgctggcatggccaaacctaacaatgatcatcagtgatgaat 200
Db 122 ggtttgccaacagaagtgaggcatggccaaagcccaacatgatcatcagcgtaaat 181
Qy 201 ggggatgatacaccattaaatctgaagtagtaccctttaaaataactgagatttccttcata 260
Db 182 ggggatttggccaccatccggtcagagagtagtacttttaaaacaccagagatttccttcaaa 241
Qy 261 ctggccaggaattgacgaagtcactcagatgacagagaagtcagaaagtcagaaatcaac 320
Db 242 ctgggctgggaattcgatgaataccacgacagacagagaagtggaaggtggaagatcataacc 301
Qy 321 ttgatgggggtgtcctgtacatgtgcagaaatgggagtgaaatcaac 370
Db 302 ctgatgtgggggcccctggtgaggtgcagagtgagagtgggatgggagaaagtcgac 351

RESULT 9
AAV10405
ID AAV10405 standard; cDNA; 411 BP.
AC AAV10405;
XX
XX
DT 26-JUN-1998 (first entry)
DE Human myelin P2 protein cDNA.
XX
XX Human; myelin; P2 protein; treatment; inflammatory polyneuritis;
KW Guillain-Barre syndrome; vasculitis; nerve inflammation;
KW gammopathy; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH 1. 411
FT CDS
FT /*tag= a
FT /transl_except= (pos:145..147, aa:Ile)
FT /product= P2_protein
XX
XX WO9803647-A2.
XX
XX 29-JAN-1998.
XX
XX 18-JUL-1997; 97WO-DE01535.
XX
XX 18-JUL-1996; 96DE-1029095.
XX
XX (GOLD/) GOLD R.
XX (WEIS/) WEISHAUP A.
XX
XX Gold R, Weishaupt A;
XX
XX WPI; 1998-120772/11.
XX P-PSDB; AAW40227.
XX
XX Recombinant myelin proteins for treating T-cell mediated disease of
XX peripheral nervous system - by high dose antigen therapy, causing
XX apoptosis in T cells, for treating e.g. polyneuritis or
XX Guillain-Barre syndrome
XX
XX Disclosure; Fig 4; 14pp; German.
XX
XX The present sequence encodes the human myelin P2 protein, which can
XX be used to treat T-cell mediated diseases of the peripheral nervous
XX system, especially chronic-inflammatory polyneuritis,
XX Guillain-Barre syndrome, vasculitis and nerve inflammation in cases
XX of gammopathy.
XX
XX Sequence 411 BP; 152 A; 80 C; 99 G; 80 T; 0 other;

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```

Query Match 33.3%; Score 211.4; DB 19; Length 411;
Best Local Similarity 71.5%; Pred. No. 3.le-53;
Matches 278; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

Qy 63 atgtgtgagctttttaggtaccttgaaacttctccagtgaaacttttgatgattat 122
Db 1 atgagcaacaattctctggcacttggaacttctctagcgaagaactttgacgattac 60
Qy 123 atgaagaagtaggagtggtcttggccaccaggaagtggtggcatggccaaacctaac 182
Db 61 atgaagctctgggtgtgggttagccaccagaaactgggaaatttggccaaacccaat 120
Qy 183 atgatcatcagtggaatggggatgtgatcaccataaattcgaagtagctttttaaata 242
Db 121 gtgatcatcagcaagaagaaggagataataactatacgaactgaagtagctttttaaata 180
Qy 243 actgagatttctctcactggtggccaggaatttgacgaagtcactgcagatgacagaaa 302
Db 181 acagaaatctctcaagtagggccaggaatttgaagaacacacagctgacaatgagaag 240
Qy 303 gtcaagagacacataaaccttagatgggggtgtcctgtgtacatgtgcagaaatgggatga 362
Db 241 accaagagcatctaaacctgcagagaggtacactgaatcaagtgcagagatgggatgac 300
Qy 363 aaatcaaccacataaagagaacagagagatgataaactggtgtggaatgcgtcatg 422
Db 301 aaagagacaacataaagaagtagtgaatgggaaatggtgagcgaatgtaaaatg 360
Qy 423 aaagcgtcacttccacgagagtttata 451
Db 361 aaggcgtgggtgcaccagaatctatga 389

RESULT 10
AAZ42917
ID AAZ42917 standard; cDNA; 276 BP.
XX
XX AC AAZ42917;
XX
XX DT 01-FEB-2000 (first entry)
XX
XX Human 5' EST isolated from a cDNA library SEQ ID NO:676.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;
XX gene therapy; chromosome mapping; upstream regulatory sequence;
XX forensic; location; development; protein synthesis; stability;
XX regulation; identification; ss.
XX
XX Homo sapiens.
XX
XX PN WO9953051-A2.
XX
XX PD 21-OCT-1999.
XX
XX PF 09-APR-1999; 99WO-IB00712.
XX
XX PR 09-APR-1998; 98US-0057719.
XX 28-APR-1998; 98US-0069047.
XX
XX PA (GENST ) GENSET.
XX
XX PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
XX WPI; 2000-038446/03.
XX P-PSDB; AAY65303.
XX
XX Novel secreted protein 5' expressed sequence tag sequences used in
XX diagnostic, forensic, gene therapy, and chromosome mapping procedures
XX
XX Claim 1; Page 523; 837pp; English.
XX
XX AAZ42265 to AAZ43075 represent novel 5' expressed sequence tag (EST)

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sequences, corresponding to human secreted proteins. AAY64651 to AAY65438 represent the EST-related proteins corresponding to AA242265 to AA243052. The 5' ESTs can be used for producing secreted human gene products. They can be used to identify and isolate 5' untranslated regions (UTRs) and upstream regulatory regions which control the location, development stage, rate, and quantity of protein synthesis, as well as stability of mRNA. The ESTs are also useful as probes for chromosome mapping, and to obtain full length cDNA clones. The ESTs can also be used in forensic procedures to identify individuals, or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal gene expression. The products may also be used in gene therapy protocols. The nucleic acids encoding signal peptides can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell. The proteins encoded by the EST sequences may be useful in treating a variety of human conditions. Secreted proteins have therapeutic value, and the identification of new secreted proteins is valuable. AA242249 to AA242264 and AAY64644 to AAY64650 represent sequences used in the exemplification of the present invention.

Sequence 276 BP; 77 A; 71 C; 59 G; 69 T; 0 other;

Query Match 32.3%; Score 205; DB 21; Length 276;

Best Local Similarity 97.7%; Pred. No. 2.1e-51;

Matches 208; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 6 tccaggagggtgcagcttccttcaccttgaaagaaataatcctagaaaaactcacaaaaatg 65  
|||||  
Db 13 tectgaaactgcagcttccttcaccttgaaagaaataatcctagaaaaactcacaaaaatg 72  
Qy 66 tctgatgtctttttaggttaccttgaaactgtctccagtgaaactttgatgattatg 125  
|||||  
Db 73 tctgatgtctttttaggttaccttgaaactgtctccagtgaaactttgatgattatg 132  
Qy 126 aaagaagtaggagtggtgttttgcaccaggaagtggtgcatgcccacacctaactg 185  
|||||  
Db 133 aaagaagtaggagtggtgttttgcaccaggaagtggtgcatgcccacacctaactg 192  
Qy 186 atcatcagtgtaatgggggtggtgatccatt 218  
|||||  
Db 193 atcatcagtgtaatgggggtggtgatccatt 225

RESULT 11

AAK86453

ID AAK86453 standard; cDNA: 374 BP.

XX AAK86453;

XX 01-MAR-2001 (first entry)

XX Mouse Ng-119K123 gene.

XX Growth hormone; brown adipose tissue; ds.

XX Mus sp.

XX WO200066784-A2.

XX 09-NOV-2000.

XX 05-MAY-2000; 2000WO-US12145.

XX 05-MAY-1999; 99US-0132670.

XX (UYOH-) UNIV OHIO.

XX Kopchick JJ, Li Y;

XX WPI; 2000-665338/64.

XX Diagnosis of abnormal levels of growth hormone in brown adipose tissue

PT is carried out by monitoring the transcriptional activity of one or  
XX more genes related to growth hormone activity -  
XX Disclosure; Page 59; 89pp; English.

XX The present invention provides a method of diagnosing abnormal levels of  
CC growth hormone (GH) in brown adipose tissue, by assaying the levels of  
CC specific gene transcripts. The genes of interest are those encoding  
CC glucosylphosphate isomerase, neuroleukin, pyruvate kinase, haem oxygenase,  
CC ubiquitin/ribosomal fusion protein, alpha-enolase, proteasome theta  
CC chain, trans-Golgi network protein, medium chain acyl-CoA dehydrogenase,  
CC adipocyte lipid binding protein, mitochondrial cytochrome C oxidase,  
CC mitochondrial NADH-ubiquinone oxidoreductase, mitochondrial cytochrome B  
CC or any of the genes Ng-119K2, Ng-119K15, Ng-119K36, Ng-119K62,  
CC Ng-119K42, Ng-119K58, Ng-119K65 or Ng-119K66. This is useful for  
CC diagnosing abnormal levels of GH or predicting changes in brown adipose  
XX tissue.

XX Sequence 374 BP; 130 A; 53 C; 93 G; 98 T; 0 other;

Query Match 32.0%; Score 203; DB 21; Length 374;

Best Local Similarity 78.3%; Pred. No. 9.7e-51;

Matches 281; Conservative 0; Mismatches 75; Indels 3; Gaps 3;

Qy 270 gaatttgacgaagtccactgcagatgcaggaagtcagagaccataacaccttagatggg 329  
|||||  
Db 1 gaatttcgatgaataccacgcagacaggaagtggaagacatcataacaccttagatggc 60  
Qy 330 ggtgtcctcgttacatgtgcagaaatgggatggaaatacaaccacataaagagaaaacga 389  
|||||  
Db 61 ggggcccctggtgcaggtgcagaaatgggatggaaatgcacacataaagagaaaacga 120  
Qy 390 gagatgataaactggtgtggaatgcgtcatgaagcgtcacctccacagagattat 449  
|||||  
Db 121 gatggtgcagacgtggtgtggaatggttatgaaagcgtgacctccacagagattat 180  
Qy 450 gagagagacataagccaagggcgcttgacctggaactgaagctgcattgacacctcacaca 509  
|||||  
Db 181 gaaagggcatgagccaaaggaag-aggcctggatggaattgcatcaaacactacaata 239  
Qy 510 tctgtgggatatattgttcaaaaagata-ttgttgttttccctgatttagcaagcaagt 568  
Db 240 gtcagtcggattattgttttttttaagatatgatttccactaataaagcaagcaatt 299  
Qy 569 aattttctcccaagctg-atatttattcaatattggttacgttggttaataaactttttt 626  
Db 300 aatttttctgaagatgcattttattgttgatatggttattgttgatttaataaactttt 358

RESULT 12

AAK53474/C

ID AAK53474 standard; cDNA: 366 BP.

XX AAK53474;

XX 16-NOV-2001 (first entry)

XX Murine transport and binding associated protein encoding cDNA SEQ ID 39.

XX Murine; liver; gene library; amino acid synthesis; binding protein;  
KW cell metabolism; energy metabolism; fatty acid metabolism; synthesis;  
KW phospholipid metabolism; purine; pyrimidine; nucleoside; nucleotide;  
KW replication; transcription; translation; transport protein; ss.

XX Mus musculus.

XX DE20103510-U1.

XX 07-JUN-2001.

XX 28-FEB-2001; 2001DE-2003510.



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PR 02-DEC-1999; 99DE-1058160.
XX (LION-) LION BIOSCIENCE AG.
XX WPI; 2001-368570/39.
XX Gene library containing sequences with specific 3'-ends and no polyA
XX tail, encoding proteins involved in a wide range of cellular processes
XX
XX Claim 15; Page 38; 251pp; German.
XX
XX This invention describes a novel gene library (A) comprises a gene
XX sequence (or its part) encoding a protein involved in amino acid
XX synthesis, cellular/energy metabolism, metabolism of
XX fatty acids/phospholipids, synthesis or breakdown of
XX purines/pyrimidines/nucleosides/nucleotides, DNA
XX replication/transcription/translation, or is a transport/binding protein.
XX (A) are produced that correspond to the 3'-end of mRNA but without the
XX polyA tail. They can be prepared more efficiently and with less effort
XX than conventional libraries. AAK53436-AAK54275 represent fragments of the
XX gene library described in the method of the invention.
XX
XX Sequence 366 BP; 99 A; 92 C; 52 G; 123 T; 0 other;
XX
XX
XX Query Match 31.7%; Score 201; DB 22; Length 366;
XX Best Local Similarity 78.2%; Pred. No. 3.8e-50;
XX Matches 279; Conservative 0; Mismatches 75; Indels 3; Gaps 3;
XX
XX QY 272 atttgacaaagtctcagatgacagaaagtcaagagcaccataacaccttagatgggg 331
XX DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 366 ATTCTGAAATCACCAGCAGCAGCAGGAAGTGAAGAGCATCATACCCCTAGATGGCGG 307
XX QY 332 tgtcttggtacatgtgcgaaatggatggaaatacaaccaccataaagagaaacgaga 391
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XX 306 GCCCTGTGCGAGGTCAGAGTGGATGGAAAGTCGACCACAAATAAGAGAAACGAGA 247
XX QY 392 ggatataaactggtggtggaatgcgtcatgaaaggcgtcactccacgagagttatga 451
XX DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 246 TGGTGACAAAGTGTGTGGTGAATGTGTATGAAAGCGTGACTCCACAAGAGTTTATGA 187
XX QY 452 gagacataagccaaggacgttgaactggactgaagttcgcattgaactctacaacatt 511
XX DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 186 AAGGCATGAGCCCAAGGAAG-AGCCCTGGATGGAAATTTGCATCAACACTACATAAGT 128
XX QY 512 ctgtgggatatattgtcaaaaagata-ttgttgttttccctgatttagcaagcaagtaa 570
XX DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 127 CAGTCGGATTTATTCTTTTAAAGATATGATTTTCCACTAATAAGCAAGCAATTAA 68
XX QY 571 ttttccccaagctg-atttattcaatatggttacgttgggttaataactttttt 626
XX DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 67 TTTTCTGAAAGATGCATTTTATTGGATATGTTATGTTGATTAATAAATAAACCTTTT 11
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XX RESULT 13
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XX ID AAC03853 standard; cDNA; 493 BP.
XX AC AAC03853;
XX AC AAC03853;
XX DT 06-OCT-2000 (first entry)
XX DE Human secreted protein 5' EST, SEQ ID NO: 3851.
XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping; ss.
XX OS Homo sapiens.
XX PN EP1033401-A2.
XX PD 06-SEP-2000.
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XX 21-FEB-2000; 2000EP-0200610.
XX 26-FEB-1999; 99US-0122487.
XX (GEST ) GENSET.
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX WPI; 2000-500381/45.
XX P-PSDB; AAG03847.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX Claim 1; SEQ ID 3851; 71pp + CD-ROM; English.
XX
XX The present sequence is one of a large number of 5' ESTs derived from
XX mRNAs encoding secreted proteins. An ORF has been identified within the
XX sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
XX derived from 30 different tissues. EST sequences usually correspond
XX mainly to the 3' untranslated region (UTR) of the mRNA because they are
XX often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
XX well suited for isolating cDNA sequences derived from the 5' ends of
XX mRNAs and even in those cases where longer cDNA sequences have been
XX obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
XX mRNAs with intact 5' ends and can therefore be used to obtain full length
XX cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
XX gene therapy and chromosome mapping procedures. They are used to obtain
XX upstream regulatory sequences and to design expression and secretion
XX vectors.
XX
XX Sequence 493 BP; 163 A; 98 C; 120 G; 110 T; 2 other;
XX
XX
XX Query Match 30.6%; Score 194; DB 21; Length 493;
XX Best Local Similarity 71.5%; Pred. No. 5.5e-48;
XX Matches 266; Conservative 2; Mismatches 102; Indels 2; Gaps 1;
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XX QY 59 caaagtgtgatgctttttgttagttacctggaacttgtctccagtgaaaactttgatga 118
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XX 116 cagatgagcaaaattcctcctggcactggaaacttgtctctagtgaactttgacga 175
XX QY 119 ttatatgaaagatgagtgagggtgttgcaccaggaagtggtggtgcattggccaacc 178
XX DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 176 ttacatgaaagctctgggtgtgggttagccaccagaaactgggaaatttggccaacc 235
XX QY 179 taacatgatcatcagtggaatggggatgtgacaccattaaactgaagtcacctttaa 238
XX DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 236 cactgtgatcatcagcaagaaaggagattataactatacgaactgaagtcacctttaa 295
XX QY 239 aaatactgagattctctcactactggccaggaatttgacgaagtcactgcagatgacag 298
XX DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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XX QY 299 gaaagtcaagagcaccataaacttagatgggggtgtcctgtgtacatgtgcagaatggga 358
XX DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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XX QY 359 tggaaaaatacaccaccataaagagaaacgagagatgataaactggtggtgaatgcgt 418
XX DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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XX QY 419 catgaaaggcgt 430
XX DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 474 aatgaaggcgt 485
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XX RESULT 14
XX AAX32482
XX ID AAX32482 standard; DNA; 8144 BP.
XX
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 8, 2002, 05:58:17 ; Search time 2258.96 Seconds  
(without alignments)  
5873.244 Million cell updates/sec

Title: US-09-503-596-2  
Perfect score: 634  
Sequence: 1 ggaattccaggagggtgcag.....ataacttttttagatttag 634

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues  
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
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Maximum Match 100%  
Listing first 45 summaries

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4: gb_on.*	483.6	76.3	619	10	AF327855
5: gb_ov.*	438	69.1	625	4	BTATFABP
6: gb_pat.*	417.8	65.9	573	4	SSC416020
7: gb_ph.*	386.2	60.9	614	10	MUSLBP
8: gb_pl.*	341.6	53.9	600	10	AF144756
9: gb_pr.*	341.6	53.9	542	10	MUS13KMP
10: gb_ro.*	313.4	49.4	395	6	A98023
11: gb_sts.*	298.2	47.0	399	10	RNU75581
12: gb_sy.*	295.8	46.7	339	4	AF136241
13: gb_vl.*	249.6	39.4	296	4	AF102872
14: gb_vl.*	240	37.9	472	5	AF432506
15: em_ba.*	232	36.6	1836	4	RABPLP2
16: em_fun.*	215.8	34.0	2150	9	HSP2RNA
17: em_hum.*	211.4	33.3	411	6	A92933
18: em_in.*	211	33.3	165948	9	AC018616
19: em_mu.*	211	33.3	174404	2	AC013542
20: em_om.*	203	32.0	374	6	AX046512
21: gb_ba.*	174.2	27.5	561	10	RNU07870
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23: gb_in.*	171.2	27.0	666	10	RATFABPH
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25: gb_ov.*	169.6	26.8	652	10	RATFABPHA
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28: gb_pl.*	166.2	26.2	701	10	BC002082
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31: gb_sts.*	164.6	26.0	1778	10	MMU02885
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33: gb_vl.*	164	25.9	705	5	AF237712
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ALIGNMENTS

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LOCUS	AX333018	Sequence 3527 from Patent WO0194629.				
DEFINITION	AX333018					
ACCESSION	AX333018.1	GI:18123652				
VERSION	AX333018.1					
KEYWORDS	human.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	1	(sites)				
AUTHORS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
TITLE	Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrikan, S., Soppet, D.R. and Weaver, Z.					
JOURNAL	Cancer gene determination and therapeutic screening using signature gene sets					
FEATURES	Patent: WO 0194629-A 3527 13-DEC-2001; Avalon Pharmaceuticals (US)					
source	Location/Qualifiers					
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	DB	ID	Description
No.	Score	Match	Length	DB	ID		



LOCUS BC003672 666 bp mRNA linear PRI 12-JUL-2001  
DEFINITION Homo sapiens, fatty acid binding protein 4, adipocyte, clone  
MGC:12293 IMAGE:3683235, mRNA, complete cds.  
ACCESSION BC003672  
VERSION BC003672.1 GI:13277535  
KEYWORDS MGC.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 666)  
Strausberg, R.  
Direct Submission  
Submitted (28-FEB-2001) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
COMMENT Contact: MGC help desk  
Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
R. M.  
Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 16 Row: m Column: 7  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 4557578.  
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Matches 612; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
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LOCUS AF327855 619 bp mRNA linear ROD 14-JAN-2002  
DEFINITION Sperophilus tridecemlineatus adipose-type fatty acid-binding  
protein (FABP4) mRNA, complete cds.  
ACCESSION AF327855  
VERSION AF327855.1 GI:12802819  
KEYWORDS thirteen-lined ground squirrel.  
SOURCE Sperophilus tridecemlineatus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;  
Sperophilus.  
REFERENCE 1 (bases 1 to 619)  
AUTHORS Hittel, D. and Storey, K.B.  
TITLE Differential expression of adipose- and heart-type fatty acid  
binding proteins(1) in hibernating ground squirrels  
JOURNAL Biochim. Biophys. Acta 1522 (3), 238-243 (2001)  
MEDLINE 21638064  
PUBMED 11779641  
REFERENCE 2 (bases 1 to 619)  
AUTHORS Hittel, D.S. and Storey, K.B.  
TITLE Direct Submission  
JOURNAL Submitted (12-DEC-2000) Biology, Carleton University, 1125 Colonel  
By Drive, Ottawa, ON K1S 5B6, Canada  
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Location/Qualifiers  
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DEFINITION (FABP4 gene).  
ACCESSION AJ416020.1 GI:16304809  
VERSION adipocyte fatty acid-binding protein; FABP4 gene.  
KEYWORDS SOURCE  
ORGANISM pig.  
Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
REFERENCE 1 (bases 1 to 573)  
AUTHORS Gerbens, F.  
TITLE Genetic control of intramuscular fat accretion in pigs. The role of heart and adipocyte fatty acid-binding proteins  
JOURNAL Thesis (2000) Department of Biochemistry MW, University of Nijmegen, Nijmegen, Netherlands  
REFERENCE 2 (bases 1 to 573)  
AUTHORS Gerbens, F., Jansen, A., van Erp, A.J., Harders, F., Meuwissen, T.H., Rettenberger, G., Veerkamp, J.H. and te Pas, M.F.  
TITLE The adipocyte fatty acid-binding protein locus: characterization and association with intramuscular fat content in pigs  
JOURNAL Mamm. Genome 9 (12), 1022-1026 (1998)  
MEDLINE 99099248  
REFERENCE 3 (bases 1 to 573)  
AUTHORS Gerbens, F.  
TITLE Direct Submission  
JOURNAL Submitted (04-OCT-2001) Gerbens F., Animal Sciences, ID-Lelystad, P.O. Box 65, NL-8200AB, NETHERLANDS  
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LOCUS Mouse 3T3-L1 lipid binding protein mRNA, complete cds.  
DEFINITION  
ACCESSION K02109  
VERSION K02109.1 GI:198716  
KEYWORDS lipid binding protein.  
SOURCE Mouse 3T3-L1 adipocytes, cDNA to mRNA, clone pAL422.  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 614)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Bernlohr, D.A., Angus, C.W., Lane, M.D., Bolanowski, M.A. and Kelly, T.J.  
TITLE Expression of specific mRNAs during adipose differentiation:  
Identification of mRNA encoding a homologue of myelin P2 protein  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 81, 5468-5472 (1984)  
MEDLINE 84298159  
COMMENT The sequence of pAL422 (422 protein) is 69% homologous to rabbit myelin P2 protein and 64% homologous to bovine myelin P2 protein, which suggests that 422 protein is an analog of myelin P2. Additional homologues with fatty acid binding proteins from rat liver and rat intestine suggest that 422 protein may be a lipid transport protein in adipocytes, and myelin P2 proteins may function similarly in Schwann cells.  
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translation="MCDAFVGTWKLVSSENFDDYMKVGVGFATPKVAGMAKPNLIIS  
VNGDLVTRSESTFKNTEISFKLGVEFDEITADRRKVKSIITLDGGALVQVKWDGKS

BASE COUNT 190 a 107 c 158 g 159 t  
ORIGIN 250 bp upstream of EcoRI site.

PUBMED 10318917  
REFERENCE 2 (bases 1 to 600)  
AUTHORS Shen, W.-J., Sridhar, K., Bernlohr, D.A. and Kraemer, F.B.  
TITLE Direct Submission  
JOURNAL Submitted (21-APR-1999) Medicine, Stanford University, S-005, Stanford, CA 94305-5103, USA  
FEATURES Location/Qualifiers  
1..600  
source

Query Match 60.9%; Score 386.2; DB 10; Length 614;  
Best Local Similarity 79.4%; Pred. No. 3.5e-89;  
Matches 482; Conservative 0; Mismatches 123; Indels 2; Gaps 2;

QY 21 ctccctctcaccttggaagaataatctcagaaactcacaaatgtgtgatgtttgtga 80  
DB 2 CTTTCTCACTGGAACACACACCTCTCTCGAAGTTTACAAATGTGTATGCTTTGTG 61  
QY 81 gttacctgaaacctctctccagtgaaaactttgatttatatatgaaagaagtagtg 140  
DB 62 GGAACCTGGAAGCTTGTCTCCAGTGAACACTTCGATGATTACATGAAGAAGTGGGAGTG 121  
QY 141 ggccttgcacaggaagtgctgcctgagccaaacctaaatgatacatcagtggaat 200  
DB 122 GCGTTTGGCCACAGGAAGTGGCAGGCTGGCCAGCCCAACATGATCATCAGCGTAAAT 181  
QY 201 gggatgtgatcaccaataaactgaaagtacacctttataaaactactgagattcttcata 260  
DB 182 GGGGATTGGTCACCATCCGGTCAGAGAGTACTTTTAAACACACCGAGATTTCCTTCAAA 241  
QY 261 ctgggcccagaatttgacgaagtcactgcagatgacaggaagtcgaagcaccataacc 320  
DB 242 CTGGCGTGGAAATTCGATGAATACCGCGACGACAGGAAAGTGGAAGCATCAATACG 301  
QY 321 ttatagtggggtgctctgtacatgctgcagaaatggatggaaatcaaccaccataaag 380  
DB 302 CTAGATGGCGGGCCCTGTGTGAGGTCAGAGTGGGAAGTGGAAATGTCGACCAATAAG 361  
QY 381 agaaacagagagatgataaaactgggtgggaatgcgtcatgaaagcgctcactccacg 440  
DB 362 AGAAACGAGAGTGTGACAAAGCTGGTGGTGAATGTGTTATGAAAGCGGTGACTTCCACA 421  
QY 441 agagtttatgagagacataaaggaagcgttgacctggagctgaagttcgactgaac 500  
DB 422 AGAGTTTATGAAGGCGCATGAGCCAAAGGAAG-AGGCCCTGGATGGAAATTTGCATCAAA 480  
QY 501 tctacaacattctgtgggtatatgttccaaaagatatgttttccctgatttaac 560  
DB 481 ACTACANTAGTCAGTCGGATTTATGTTTTTTTAAAGATATGATTTTCCACTAATAAGC 540  
QY 561 aagcaagtaattctcccgaactg-atatttccaatatggttaactgttggttaataaac 619  
DB 541 AAGCAATTAATTTTCTCAAGATGCATTTTATTGGATATGCTTATGTTGATTAAATAA 600  
QY 620 ttttttt 626  
DB 601 ACCTTTT 607

RESULT 8  
AF144756 600 bp mRNA linear ROD 07-JUN-1999  
LOCUS Rattus norvegicus adipocyte lipid-binding protein (ALBP) mRNA,  
DEFINITION complete cds.  
ACCESSION AF144756  
VERSION AF144756.1 GI:5002227  
KEYWORDS Norway rat.  
SOURCE Rattus norvegicus  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus  
1 (bases 1 to 600)  
Shen, W.-J., Sridhar, K., Bernlohr, D.A. and Kraemer, F.B.  
TITLE Interaction of rat hormone-sensitive lipase with adipocyte  
lipid-binding protein  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (10), 5528-5532 (1999)  
MEDLINE 99254074

10318917  
2 (bases 1 to 600)  
Shen, W.-J., Sridhar, K., Bernlohr, D.A. and Kraemer, F.B.  
Direct Submission  
Submitted (21-APR-1999) Medicine, Stanford University, S-005, Stanford, CA 94305-5103, USA  
Location/Qualifiers  
1..600  
source  
/organism="Rattus norvegicus"  
/strain="Sprague Dawley"  
/db\_xref="taxon:10116"  
/tissue\_type="adipose tissue"  
1..600  
/gene="ALBP"  
54..506  
/gene="ALBP"  
/note="fatty acid binding protein"  
/codon\_start=1  
/product="adipocyte lipid-binding protein"  
/protein\_id="AAD37371.1"  
/db\_xref="GI:5002228"  
/translation="MCDAPVGTWKLVSSENFDDYMKVGVGFATRKVAMAKPNLIIS  
VEGDLVIRSESTFKNTSEISPLKGVFEIDPDRKVKSIITLDGVLVHVQKWDGKS  
TTIKRRXGDKLVCEVVKGVTSRVYRAXAKRGKGLKFSASNTII"  
BASE COUNT 170 a 112 c 160 g 149 t 9 others  
ORIGIN  
Query Match 53.9%; Score 341.8; DB 10; Length 600;  
Best Local Similarity 82.1%; Pred. No. 9.9e-78;  
Matches 391; Conservative 0; Mismatches 85; Indels 0; Gaps 0;  
QY 43 aatctcagaaactcacaaatgtgtgatgtcttttagtacctggaactgtctcca 102  
DB 34 AGTCCTTGAAGCTTACAAATGTGCGACGCTTTTGGGGACCTGGAACTCGTCCA 93  
QY 103 gtgaacttttgatttatgaaagaagtaggagtggttggccaccaggaagtgg 162  
DB 94 GTGAGAACTTCGATGATTACATGAAGAAGTGGGAGTTGGCTTGGCCACCAGGAAGTGG 153  
QY 163 ctggcatggccaaacctaaacatgacatcagtggaatgggagtgatgatacattaaat 222  
DB 154 CCGGTATGCCAAGCCCAACTTGATCATCAGCGTAGAAGGGGACTTGGTCGTCATCCGGT 213  
QY 223 ctgaagtagcttttaaaatactgagatttcttcatactggtggccagggaattgacgaag 282  
DB 214 CAGAGAGTACTTTTAAACACACCGAGATTCTTCAAACTGGCGTGGAAATTCGATGAAA 273  
QY 283 tcaactgcagatgacaggaagtcgaagagcaccataacaccttagatgggtgtctctgtac 342  
DB 274 TCACCCAGATGACAGGAAAGTGAAGAGCATCATAAACCTGGATGTTGGGGTCTCGGTAC 333  
QY 343 atgtgcagaaatggatggaaaatacaaccaccataaagaaagagagagatgataaac 402  
DB 334 ATGTGCAAGTGGGATGGAAGTGCACCCATTAAGAGGAGAGNAGATGTTGACAAGC 393  
QY 403 tgggtggtgaatgcgtcatgaaagcgtcacttcaccagagagtttatgagagagcataag 462  
DB 394 TGGTGGTGAAGTGTCTCATGAAAGCGGTGACATTCCTACAGAGCTTTACNAAAGGCGATNAG 453  
QY 463 ccaagggacgttgacctggactgaagttgcattgaactctacaacattctgtggg 518  
DB 454 CCAAGGGACGAGGCCCTGGACTGAAATTTGCATCAAACTCTACAATAACTTGTATGG 509  
RESULT 9  
MUS13KMP 542 bp mRNA linear ROD 27-APR-1993  
LOCUS Mouse 13K protein mRNA, 3' end.  
DEFINITION M28726  
ACCESSION M28726  
VERSION M28726.1 GI:191492  
KEYWORDS 13 kDa protein.  
SOURCE Mouse 3T3-adipocyte cell line, cDNA to mRNA.



**ORGANISM** Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
**REFERENCE** 1 (bases 1 to 542)  
 Cook, K.S., Hunt, C.R. and Spiegelman, B.M.  
**AUTHORS** Developmentally regulated mRNAs in 3T3-adipocytes: Analysis of  
**TITLE** transcriptional control  
**JOURNAL** J. Cell Biol. 100, 514-520 (1985)  
**MEDLINE** 85105214  
**FEATURES**

Location/Qualifiers	
1..542	
/organism="Mus musculus"	
/db_xref="taxon:10090"	
/cell_line="3T3"	
/cell_type="adipocyte"	
<1..542	
/product="13k protein"	
<1..369	
/codon_start=1	
/product="13k protein"	
/protein_id="AAA37112.1"	
/db_xref="GI:191493"	
/translation="LVSENFDDYKVEGVGTRKRVAGMAKPNMIISVNGDLVTIIRS ESTFKNTEISFLGVSEFDITADDRKVKSIITLDGGALYQVQKWDGKSTTIKRKRDDG KLWVECMKGVSTSTRYERA"	

**BASE COUNT** 173 a 90 c 140 g 139 t  
**ORIGIN**

Query Match	53.9%;	Score	341.6;	DB 10;	Length	542;
Best Local Similarity	81.0%;	Pred. No.	1.1e-77;			
Matches	434;	Conservative	0;	Mismatches	99;	Indels 3; Gaps 3;

  

QY	93	cttgtctccagtgaaaacttggattgattatgataaagaagtagagtgggctttggccacc	152
Db	1	CTTGCTCCAGTGAACACTTCGATGATTACATGAAGAAGTGGAGTGGCTTTGCCACA	60
QY	153	agaaagtggtgctggcattggtggccaaacctacaatgatcatcagtgtaatggggatgtgatc	212
Db	61	AGGAAGTGGCAGCATATGGCCATATGACCAAGCCCAACATGATCATCAGCGTAATATGGGGATTGGTC	120
QY	213	accattaaatctgaagtcacctttaaaatactgagagattccctcactacggtggccagaa	272
Db	121	ACCATCCGGTCAGAGAGTACTTTTAAAAACACCGAGATTTCCITCAAACTGGGCGTGGAA	180
QY	273	tttgacgaagtcactgcagatgacaggaagtcacagagcaccataacacttagatgggggt	332
Db	181	TTTCGATGAAATCATCCGCAGACGACAGGAAGTGGAAGAGCATCATTAACCTAGATGGCGGG	240
QY	333	gtcctggtacatgtgcagaataatggatggaaaatacaaccaccataaagagaaacagag	392
Db	241	GCCCTGTGTCAGGTGCGAAGAGTGGGATGGGAATGCGACCAATTAAGAGAAAACGAGAT	300
QY	393	gatgataaactggtgtggtaatgcgtcatgaaagcgctcaactccacgagagtttatgag	452
Db	301	GGTGACAAGCTGGTGTGGAATGTGTTATGAAGGCGTGACTTCCACAAGAGTTTATGAA	360
QY	453	agagcataagccaagggaactgtgaactggactgaagtcgcattggaactctacaacattc	512
Db	361	AGGCGATAGGCCCAAGGAAG-AGGCGCTGGATGGGAATTTGCATCAAAACATCAATAATGTC	419
QY	513	tgtgggataattgttccaaaaagata-ttgttgtttccctgatttagcaagcaagttaatt	571
Db	420	AGTCGGATTATGCTTTTTTTTTTAAAGATATGATTTTCCACTAATATAGCAAGCAATTAAT	479
QY	572	tttctcccaagctg-atatttattcaatgatggttcacgttggtgtaataactttttt	626
Db	480	CTTTTCTGAAGATGCATTTTATTTGGATTTGGTATGTTGTTGTTAATAATAAAACCTTTT	535

RESULT	10			
A98023				
LOCUS	A98023	395 bp	DNA	linear
				PAT 26-JAN-2000

DEFINITION	Sequence 2 from Patent WO9914365.
ACCESSION	A98023
VERSION	A98023.1
KEYWORDS	GI:6781261
SOURCE	unidentified.
ORGANISM	unidentified.
REFERENCE	unclassified.
AUTHORS	1 (bases 1 to 395)
TITLE	THE PORCINE ADIPOCYTE FATTY ACID-BINDING PROTEIN ENCODING GENE AND METHODS TO LOCALISE, IDENTIFY OR MARK GENES OR ALLELES OR QUANTITATIVE TRAIT LOCI OF FARM ANIMALS
JOURNAL	Patent: WO 9914365-A 2 25-MAR-1999;
FEATURES	STAMBOEK ZUID B V (NL); DALLAND B V (NL)
source	Location/Qualifiers
	1..395
	/organism="unidentified"
	/db_xref="taxon:32644"
BASE COUNT	132 a 67 c 105 g 91 t
ORIGIN	
Query Match	49.4%; Score 313.4; DB 6; Length 395;
Best Local Similarity	90.0%; Pred.No. 2.1e-70;
Matches 359; Conservative	0; Mismatches 36; Indels 4; Gaps 2;
Qy	63 atgtgtatgctttttagtgacctggaacattctccagtgaaaactttgatgattat 122
Db	1 ATGTGTATGTCATTTGTAGGTACCT-GAAACTTCTCCAGTGAAAACCTTTGATGATTAC 59
Qy	123 atgaagaagtagagtgaggctttgcccacaggaagaagtggctgcatggccaaacacctaac 182
Db	60 ATGAAGAAGTGGGAGTGGGCTTTGCCACCAGGAAGTGGCTGGCATGGCCAAACCCCAAC 119
Qy	183 atgatcatcagtggaatgggagtgatcaccattaaactgaaagtacacttttaaaaaat 242
Db	120 CTGATCATCACTGTGAATGGGGATATGATCACCATTAGATCAGAAAGTACCTTTTAAAAAT 179
Qy	243 actgagatctcttcatactggccaggaatttgacgaagtcaactgcagatgcagagaaa 302
Db	180 ACTGAGATTGCTTCAAAATTGGCCAGCAAAATTCATGAAGTCACTGCAGATGACAGGAAA 239
Qy	303 gtcagagcaccataaacttagatgggggtgtcctgtacatgtgcagaaatgggagtggga 362
Db	240 GTCAAGAGCACATAAACCCTTAGATGGAGGCCCTGGTGTACAGGTGCAGAACTGGGATGGA 299
Qy	363 aaatcaaccaccataaagagaaaacagagatgataaactggtggtggaatgcgtcatg 422
Db	300 AAGACACCACCATTAACAGAAAAATA---GTAGATGAATGGTGGTGGGAATGATCATG 356
Qy	423 aaagcgtcacttcacagagagatttatgagagacataa 461
Db	357 AAGGTGTACGGCTACCAGAAATTTATGAGAGACATAA 395
RESULT 11	
RNU75581	399 bp mRNA linear ROD 23-MAR-2001
LOCUS	Rattus norvegicus adipocyte fatty acid binding protein (A-FABP)
DEFINITION	mRNA, complete cds.
ACCESSION	U75581
VERSION	U75581.1
KEYWORDS	GI:1658524
SOURCE	Norway rat.
ORGANISM	Rattus norvegicus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
TITLE	Rattus.
	1 (bases 1 to 399)
	Prinsen,C.F. and Veerkamp,J.H.
	transfection of L6 myoblasts with adipocyte fatty acid-binding
	protein cDNA does not affect fatty acid uptake but disturbs lipid
	metabolism and fusion

REFERENCE  
1 (bases 1 to 399)  
AUTHORS  
Prinsen,C.F. and Veerkamp,J.H.  
TITLE  
Transfection of L6 myoblasts with adipocyte fatty acid-binding  
protein cDNA does not affect fatty acid uptake but disturbs lipid  
metabolism and fusion

JOURNAL Biochem. J. 329 (Pt 2), 265-273 (1998)  
MEDLINE 98087494  
PUBMED 9425108  
REFERENCE 2 (bases 1 to 399)  
AUTHORS Prinsen, C. and Veerkamp, J.  
TITLE Direct Submission  
JOURNAL Submitted (22-OCT-1996) Dept. Biochemistry, University of Nijmegen,  
Adelbertusplaats 1, Nijmegen 6500 HB, The Netherlands  
FEATURES Location/Qualifiers  
source 1..399  
/organism="Rattus norvegicus"  
/db\_xref="taxon:10116"  
1..399  
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/gene="A-FABP"  
/codon\_start=1  
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/protein\_id="AAB18344.1"  
/db\_xref="GI:1658525"  
/translation="MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNLIIS  
VEGLDVIRSESTFKNTEISFKLGVEDEITPDRKVKSIITLDGGVLVHVOKWDGKS  
TTIKRQDGLVVECYMKGVTSTVVERA"  
BASE COUNT 118 a 73 c 119 g 89 t  
ORIGIN

Query Match 47.0%; Score 298.2; DB 10; Length 399;  
Best Local Similarity 84.2%; Pred. No. 1.8e-66;  
Matches 336; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 63 atgtgtgagcttctttagtgacacgttgaaacttgcctccagtgaaactttagtattat 122  
Db 1 ATGTGTGATGCTTGTGGGACCTGGAAACTCGCTCCAGTGAGAACTTCGATGATTAC 60

QY 123 atgaagaagttagtgagtgcttccaccaggaaagtggctggcagatggccaaacctaac 182  
Db 61 ATGAAGAAGTGGGAGTTGGCTTCGCCACCAGGAAGTGGCCGGTATGCCCAAGCCCAAC 120

QY 183 atgacatcagtgtaagggtgatgtatcaccattaaactgaaagtacaccttttataat 242  
Db 121 TTGATCATCAGGTAGAGGGGACTTGGTCGTCATCCGGTCAGAGAGTACTTTAAAC 180

QY 243 actgagattcttcatactactggccaggaatttgacgaagtcactgcagatgacaggaaa 302  
Db 181 ACCGAGATTTCTTCAAACTGGGTGTGAATTCGATGAATCACCACCCAGATGACAGGAAA 240

QY 303 gtcaagagacacataacctatagtggtgtcctggtacatgtgcagaaatgggatgga 362  
b 241 GTGAAGACATCATAACTCTGATGGTGGGTCTCTGGTACATGTGCAAGTGGGATGGA 300

QY 363 aaatcaacacacataaagagaaacagagagatgataaactggtggaatgcgtcatg 422  
Db 301 AAGTCGACCACCATAAAGAGACGAGAGATGCTGACAAAGCTGGTGGTGAATGTGTCATG 360

QY 423 aaagcgtcacttccacagagagtttatgagagagacataa 461  
Db 361 AAAGCGTGACTTCTACAAAGAGTTTATGAAAGAGCATAA 399

RESULT 12  
AF136241  
LOCUS AF136241 339 bp mRNA linear MAM 25-MAY-1999  
DEFINITION Oryctolagus cuniculus adipocyte lipid-binding protein (ap2) mRNA,  
partial cds.  
ACCESSION AF136241  
VERSION AF136241.1 GI:4887136  
KEYWORDS rabbit.  
SOURCE Oryctolagus cuniculus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
REFERENCE 1 (bases 1 to 399)

AUTHORS Guan, Y., Zhang, Y., Davis, L., Davis, L. and Breyer, M.D.  
TITLE Expression of ap2 gene in transitional epithelium of rabbit bladder  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 339)  
AUTHORS Guan, Y., Zhang, Y., Davis, L. and Breyer, M.D.  
TITLE Direct Submission  
JOURNAL Submitted (19-MAR-1999) Division of Nephrology, Vanderbilt  
University Medical Center, 21st street, Nashville, TN 37232-2372,  
USA  
FEATURES Location/Qualifiers  
source 1..339  
/organism="Oryctolagus cuniculus"  
/strain="New Zealand White"  
/db\_xref="taxon:9986"  
/tissue.type="bladder"  
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/protein\_id="AAD32209.1"  
/db\_xref="GI:4887137"  
/translation="TWKLVSSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVIT  
IKSESTFKNTEISFKLGQEFDEVTAADRRKKSIIITLDGGALVQVQKWDGKSTTIKRR  
EGDKLVVVECYM"  
BASE COUNT 108 a 63 c 97 g 71 t  
ORIGIN

Query Match 46.7%; Score 295.8; DB 4; Length 339;  
Best Local Similarity 92.0%; Pred. No. 7.3e-66;  
Matches 312; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 84 acctggaactgtctccagtgaaaaactttagtattatataagaagaagtagtgagggc 143  
Db 1 ACCTGGAAGCTTGTCTCCAGTGAGAACTTGTACGATTACATGAAAGAGTGGGAGTGGGC 60

QY 144 ttgcccaccaggaagtgtgctgcatggccaaacctaacatgacatcatcagttgtaagg 203  
Db 61 TTCGCCACCAGGAAGTGGTGGCATGGCCAAACCCACATGATCATCATGTGTGAATGGG 120

QY 204 gatgtgataccataataatctgaaagtacacctttaaataactagattccttcatactg 263  
Db 121 GATGTGATCACCATTAAATCAGAGAGACCTTTAAAAACACACTGAGATTTCTTCAAACTG 180

QY 264 gcccaggaatttgacgaagtcaactcagatgacagaagaagcaagaccataaccctta 323  
Db 181 GCCCAGGAATTTGATGAAGTCAACCGCAGATGACAGGAAGGCAAGAGTATCATATAACCTTA 240

QY 324 gatgggggtgctctgtgtacatgtgcagaaatgggagtggaatacaccataaagaga 383  
Db 241 GATGGTGGTCCCTGGTCCAGGTGCAGAGTGGGATGGGAATAACACACCACCATAAAGAGA 300

QY 384 aaacagagaggatgataaactggtggtggaatgcgtcatg 422  
Db 301 AAACGGGAGGTGATAAACTGGTGGTGGTGAATGTGTATG 339

RESULT 13  
AF102872  
LOCUS AF102872 296 bp mRNA linear MAM 12-APR-2000  
DEFINITION Sus scrofa adipocyte fatty acid binding protein (ap2) mRNA, partial  
cds.  
ACCESSION AF102872  
VERSION AF102872.1 GI:3907628  
KEYWORDS pig.  
SOURCE Sus scrofa  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
REFERENCE 1 (bases 1 to 296)

AUTHORS Ding S.T., McNeel, R.L. and Mersmann, H.J.  
TITLE Expression of porcine adipocyte transcripts: tissue distribution and differentiation in vitro and in vivo  
JOURNAL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 123 (3), 307-318 (1999)  
MEDLINE 99410873  
PUBMED 10481259  
REFERENCE 2 (bases 1 to 296)  
AUTHORS Ding S.T. and Mersmann, H.J.  
TITLE Direct Submission  
JOURNAL Submitted (29-OCT-1998) Pediatrics, Baylor College of Medicine, 1100 Bates St., Houston, TX 77030, USA  
FEATURES  
source Location/Qualifiers  
1..296  
/organism="Sus scrofa"  
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/protein\_id="AAC78684.1"  
/db\_xref="GI:3907629"  
/translations="GPATRKVAGMAKPNLIITVNGDMITIRSESTFKNTEIAFKLGOE  
FDEVTADDRKVKSTIILDGALVQVQKWDGKTTINKRKIVDDKLVECVNMGVTA"  
BASE COUNT 98 a 54 c 79 g 65 t  
ORIGIN

Query Match 39.4%; Score 249.6; DB 4; Length 296;  
Best Local Similarity 90.2%; Pred. No. 6.1e-54;  
Matches 267; Conservative 0; Mismatches 29; Indels 0; Gaps 0;  
QY 141 ggccttgccaccaggaagtgcgtggcatggccaaacccaacatgatcatcagtgatgaat 200  
DB 1 GCGTTTGCTACCCAGGAAGTGGCTGGCATGCCAAACCCAACTGATCATCACGTGAAT 60  
QY 201 ggggatgtgataccattaaatctgaaagtacacctttaaataactgagattccttcata 260  
DB 61 GGGGATATGATCACCATTAGATCAGAAAGTACCTTTAAATAACTGAGATTGCCCTTCAAA 120  
QY 261 ctggccagggaattgacgaagtcaactgcagatcacaggaagcaagcaagcaccataacc 320  
DB 121 TTGGCCAGGAATTTGATGAGTCACTCCAGATGACAGGAAGTCAAGAGCACCATAACC 180  
QY 321 ttataggggggtgctcctgtgacatgtgcagaaatgggagtggaataatcaaccaccataaag 380  
DB 181 TTAGATGGAGGCGCCCTGGTACAGTGCAGAAAGTGGGATGGAAGACACCAACATAAAC 240  
QY 381 agaaaacagaggagatgataaactgggtggaatgcgtcatgaaaggcgctcacttc 436  
DB 241 AGAAAAATAGTAGATGATGAAGTTGGTGGTGAATGTGTGCATGAATGTGTCACTGC 296

RESULT 14  
AF432506 472 bp mRNA linear VRT 12-NOV-2001  
LOCUS Gallus gallus adipocyte fatty acid binding protein (AFABP) mRNA,  
complete cds.  
ACCESSION AF432506  
VERSION AF432506.1 GI:16904068  
KEYWORDS chicken.  
SOURCE Gallus gallus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 472)  
AUTHORS Wang, Q., Li, N. and Li, H.  
TITLE Cloning and sequencing of adipocyte fatty acid binding protein gene in chicken

JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 472)  
AUTHORS Wang, Q., Li, N. and Li, H.  
TITLE Direct Submission  
JOURNAL Submitted (12-OCT-2001) Animal Science and Technology College, Northeast Agricultural University, Mucai Street 59, Harbin, Heilongjiang 150030, China  
FEATURES  
source Location/Qualifiers  
1..472  
/organism="Gallus gallus"  
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/tissue\_type="fat"  
/dev\_stage="adult"  
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1..472  
/gene="AFABP"  
35..433  
/gene="AFABP"  
/codon\_start=1  
/product="adipocyte fatty acid binding protein"  
/protein\_id="AAL30743.1"  
/db\_xref="GI:16904069"  
/translation="MCDQFVGTWKLSSSEFEDYMKELGVGFATRKMGVAKPNLITIS  
INGDVIIRSESTFKNTEISFKLGEFDETTADDRTKKNVITLDSGTLKQVQKWDGKE  
TVIKRKVVVDGNLLVECTMNNVTSKRVYERA"  
BASE COUNT 153 a 85 c 131 g 103 t  
ORIGIN

Query Match 37.9%; Score 240; DB 5; Length 472;  
Best Local Similarity 72.2%; Pred. No. 1.8e-51;  
Matches 312; Conservative 0; Mismatches 120; Indels 0; Gaps 0;  
QY 55 ctcaacaagtgtgtagctttttagtagtacctggaactgtctccagtgaaaactttg 114  
DB 27 CTGCAAAATGTGCGACCAAGTTTGTGGCACCTCGGAAGCTCTTTCTAGTGAACCTTTG 86  
QY 115 atgattatataaagaagtagagtggtgcttgcaccaggaagagctgcgcagatgcca 174  
DB 87 AGGACTATATGAAGAGCTGGGTGGGGTTTGCTACCAGGAAGATGGCTGTGTGGCCA 146  
QY 175 aacctaaacatgatcatcagtggaatgggagtgatgatacaccattataatctgaaagtac 234  
DB 147 AGCCTAATTAATCATCAGCATCAATGGTGATGTGATACCATCATGATCAGAAAGTACCT 206  
QY 235 ttaaaaactgtagagattccttcatactatctggcagggaatttgacgaagtcaactgcagatg 294  
DB 207 TCAAAAATACAGAGATCTCTTTCAAGCTGGGTGAAGAGTTTGTGATGAGACACAGCAGATG 266  
QY 295 acaggaagagcaagagcaccataaccttagatgggggtgctcctgtacatgtgcagaaat 354  
DB 267 ACAGAAAAACAAGAAATGTCAATACCCCTAGACAGTGGCACACTGAAGAGGTGCAGAGT 326  
QY 355 gggatggaaaaatcaaccaccataaagaaacagagagatgataaactgggtgggaat 414  
DB 327 GGGATGGCAAGAGACTGTTATCAAGAGAAAGAGTGGTGGTGGGAACCTGCTGGTGAAT 386  
QY 415 ggcgtcatgaaaggcgctcactccacgagagatttatgagagagataagccaaggagcgtt 474  
DB 387 GCACCAATGAATAATGTTACCAGCAAAAGAGTTTACGAAAGAGCATGAGGAAGCCGCTCTTC 446  
QY 475 gacctggactga 486  
DB 447 ATGTGGGACTGA 458

RESULT 15  
RABPLP2  
LOCUS RABPLP2  
DEFINITION Rabbit myelin P2 mRNA, complete cds.  
ACCESSION J03744  
VERSION J03744.1 GI:165657  
KEYWORDS myelin.

Search completed: June 8, 2002, 08:43:34  
Job time: 9917 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2002, 18:19:33 ; Search time 27.07 Seconds  
(without alignments) 843.566 Million cell updates/sec

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Title: US-09-503-596-4
Perfect score: 675
Sequence: 1 MCDAFVGTWKLVSSENFDDY.....KLWECVMKGVTSTRVYERA 132

```

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 5622222

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

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```
Database :
1:  sp_archaea.*
2:  sp_bacteria.*
3:  sp_fungi.*
4:  sp_human.*
5:  sp_invertebrate.*
6:  sp_mammal.*
7:  sp_mhc.*
8:  sp_organelle.*
9:  sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_ivirus.*
16: sp_bacteriap.*
17: sp_archaeap.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	SUMMARIES			ID	Description
	Score	% Match	Length		
1	651	96.4	132	11	Q99P60 spermophilu
2	603	89.3	150	11	Q9R290 rattus norv
3	537	78.6	113	6	Q9XS64
4	531	78.7	132	13	Q9XS94 oryctolagus
5	473.5	70.1	134	11	Q9QX56 gallus gall
6	468	69.3	133	11	Q9QX04 rattus norv
7	466	69.0	133	11	Q99P61 spermophilu
8	462	68.4	131	13	Q91W23 mus musculu
9	443	65.6	132	13	Q9QX55 gallus gall
10	433	64.1	99	6	Q9W992 fundulus he
11	427	63.3	125	6	Q97675 sus scrofa
12	413	61.2	132	13	Q9XS15 equus cabal
13	402	59.6	132	13	Q918N9 brachydanio
14	400	59.3	133	13	Q9DAL2 mus musculu
15	397	58.8	133	13	Q57668 cryodraco a
16	397	58.8	133	13	Q57667 chaenocepha
					Q57670 gobionototh

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||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 61 TEISFKLGEFDEVTADRRKVKSIITLDGGVLVQVQKWDGKSTTIKKRREDDKLVEECVM 120
QY 121 KGVTSRTRYERA 132
||||| |||||||
Db 121 KGVTSRTRYERA 132

RESULT 2
Q9R290 PRELIMINARY; PRT; 150 AA.
ID Q9R290
AC Q9R290;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ADIPOCYTE LIPID-BINDING PROTEIN.
GN ALBP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE DAWLEY; TISSUE=ADIPOSE TISSUE;
RX MEDLINE=99254074; PubMed=10318917;
RA Shen W.-J., Sridhar K., Bernlohr D.A., Kraemer F.B.;
RT "Interaction of rat hormone-sensitive lipase with adipocyte lipid-
binding protein."
RL Proc. Natl. Acad. Sci. U.S.A. 96:5528-5532(1999).
DR EMBL; AF144756; AAD37371.1; -.
DR HSP; P04117; ILID.
DR InterPro; IPR000463; Fatty_acid_BP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
SQ SEQUENCE 150 AA; 16468 MW; 9D214AB610D0C54E CRC64;

Query Match 89.3%; Score 603; DB 11; Length 150;
Best Local Similarity 87.9%; Pred. No. 2e-49;
Matches 116; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MCDFAVGTTKLVSSSENFDDYKMGVGFATRKVAGMAKPNMIIISVNGDVITIKSESTFKN 60
Db 1 MCDFAVGTTKLVSSSENFDDYKMGVGFATRKVAGMAKPNMIIISVNGDVIRSESTFKN 60

QY 61 TEISFKLGEFDEVTADRRKVKSIITLDGGVLVQVQKWDGKSTTIKKRREDDKLVEECVM 120
Db 61 TEISFKLGEFDEVTADRRKVKSIITLDGGVLVQVQKWDGKSTTIKKRREDDKLVEECVM 120

QY 121 KGVTSRTRYERA 132
||||| |||||||
Db 121 KGVTSRTRYERA 132

RESULT 3
Q9XSG4 PRELIMINARY; PRT; 113 AA.
ID Q9XSG4
AC Q9XSG4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ADIPOCYTE LIPID-BINDING PROTEIN (FRAGMENT).
GN AP2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
[1]
SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=URINARY BLADDER;
RA Guan Y., Zhang Y., Davis L., Breyer M.D.;
```

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"Expression of ap2 gene in transitional epithelium of rabbit
bladder.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF136241; AAD32209.1; -.
DR HSP; P04117; ILID.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; lipocalin_cytfABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12536 MW; 4C19A538EC897F4F CRC64;

Query Match 79.6%; Score 537; DB 6; Length 113;
Best Local Similarity 94.7%; Pred. No. 2.4e-43;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 8 TWKLVSSSENFDDYKMGVGFATRKVAGMAKPNMIIISVNGDVITIKSESTFKNTEISFIL 67
Db 1 TWKLVSSSENFDDYKMGVGFATRKVAGMAKPNMIIISVNGDVITIKSESTFKNTEISFKL 60

QY 68 GQEFDEVTADRRKVKSIITLDGGVLVQVQKWDGKSTTIKKRREDDKLVEECVM 120
Db 61 GQEFDEVTADRRKVKSIITLDGGVLVQVQKWDGKSTTIKKRREDDKLVEECVM 113

RESULT 4
Q90X56 PRELIMINARY; PRT; 132 AA.
ID Q90X56
AC Q90X56;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ADIPOCYTE FATTY ACID BINDING PROTEIN.
GN AFABP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FAT;
RA Wang Q., Li N., Li H.;
RT "Cloning and sequencing of adipocyte fatty acid binding protein gene
in chicken.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF432506; AAL30743.1; -.
SQ SEQUENCE 132 AA; 14894 MW; 4F5905FAB8DA268B CRC64;

Query Match 78.7%; Score 531; DB 13; Length 132;
Best Local Similarity 76.5%; Pred. No. 1.1e-42;
Matches 101; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

QY 1 MCDFAVGTTKLVSSSENFDDYKMGVGFATRKVAGMAKPNMIIISVNGDVITIKSESTFKN 60
Db 1 MCDFAVGTTKLVSSSENFDDYKMGVGFATRKVAGMAKPNMIIISVNGDVIRSESTFKN 60

QY 61 TEISFKLGEFDEVTADRRKVKSIITLDGGVLVQVQKWDGKSTTIKKRREDDKLVEECVM 120
Db 61 TEISFKLGEFDEVTADRRKVKSIITLDGGVLVQVQKWDGKSTTIKKRREDDKLVEECVM 120

QY 121 KGVTSRTRYERA 132
||||| |||||||
Db 121 NNVTSKRYERA 132

RESULT 5
Q9QY04 PRELIMINARY; PRT; 134 AA.
ID Q9QY04
AC Q9QY04;
```



RT "Cloning and sequencing of adipocyte fatty acid binding protein gene  
in chicken."  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF432507; AAL30744.1; -  
FT NON\_TER 111  
SQ SEQUENCE 111 AA; 12514 MW; 3B102FB5E28D2276 CRC64;

Query Match 68.4%; Score 462; DB 13; Length 111;  
Best Local Similarity 78.4%; Pred. No. 2.8e-36;  
Matches 8; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MCDAFVGTWKLVSSENFDDYKMGVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60  
Db 1 MCDQFVGTWKLVSSENFDDYKMGVGVGFATRKVAGMAKPNLTISVNGDVITIRSESTFKN 60  
Qy 61 TEISFILQGEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRRED 111  
Db 61 TEISFKLGEFDETTADDRKTKNVTLDGSLQVQKWDGKSTTIKKRVED 111

RESULT 9  
DT90W92  
Q90W92 PRELIMINARY; PRT; 132 AA.  
Q90W92

DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE HEART-TYPE FATTY ACID-BINDING PROTEIN.  
GN H-FABP.

OS Fundulus heteroclitus (Killifish) (Mummichog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;  
OC Cyprinodontiformes; Fundulidae; Fundulus.  
OX NCBI\_TaxID=8078;

RESULT 9  
DT90W92  
Q90W92 PRELIMINARY; PRT; 132 AA.  
Q90W92

Query Match 65.6%; Score 443; DB 13; Length 132;  
Best Local Similarity 62.9%; Pred. No. 2.2e-34;  
Matches 83; Conservative 20; Mismatches 29; Indels 0; Gaps 0;

Qy 1 MCDAFVGTWKLVSSENFDDYKMGVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60  
Db 1 MVEAFVGTWKLVSSENFDDYKMGVGVGFATRKVAGMAKPNLTISVNGDVITIKSESTFKN 60  
Qy 61 TEISFILQGEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDKLVVCEVM 120  
Db 61 TEISFKLGEFDETTADDRKVKSLVTIEDGKLHVHVQKWDGKSTTIKKRREDKLVVCEVM 120

Qy 121 KGVSTRVYERA 132  
Db 121 GGVVSKRRHYEKA 132

RESULT 10  
Q97675  
Q97675 PRELIMINARY; PRT; 99 AA.

DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE ADIPOCYTE FATTY ACID BINDING PROTEIN (FRAGMENT).  
GN AP2.

OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;

Qy 1 MCDAFVGTWKLVSSENFDDYKMGVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60  
Db 1 MCDQFVGTWKLVSSENFDDYKMGVGVGFATRKVAGMAKPNLTISVNGDVITIRSESTFKN 60  
Qy 61 TEISFILQGEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRRED 111  
Db 61 TEISFKLGEFDETTADDRKTKNVTLDGSLQVQKWDGKSTTIKKRVED 111

Query Match 64.1%; Score 433; DB 6; Length 99;  
Best Local Similarity 85.9%; Pred. No. 1.4e-33;  
Matches 85; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 27 GFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTEISFILQGEFDEVTADDRKVKSTIT 86  
Db 1 GFATRKVAGMAKPNMIISVNGDVITIRSESTFKNTEISFILQGEFDEVTADDRKVKSTIT 60  
Qy 87 LDGGVLVHVQKWDGKSTTIKKRREDKLVVCEVMKGVTS 125  
Db 61 LDGGVLVHVQKWDGKSTTIKKRREDKLVVCEVMKGVTS 99

RESULT 11  
Q9XSIS  
Q9XSIS PRELIMINARY; PRT; 125 AA.

DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE HEART-TYPE FATTY ACID-BINDING PROTEIN (FRAGMENT).  
GN FABP3.

OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796;

Qy 1 MCDAFVGTWKLVSSENFDDYKMGVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60  
Db 1 MVEAFVGTWKLVSSENFDDYKMGVGVGFATRKVAGMAKPNLTISVNGDVITIKSESTFKN 60  
Qy 61 TEISFILQGEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDKLVVCEVM 120  
Db 61 TEISFKLGEFDETTADDRKVKSLVTIEDGKLHVHVQKWDGKSTTIKKRREDKLVVCEVM 120

Qy 121 KGVSTRVYERA 132  
Db 121 GGVVSKRRHYEKA 132

RESULT 10  
Q97675  
Q97675 PRELIMINARY; PRT; 99 AA.

DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE ADIPOCYTE FATTY ACID BINDING PROTEIN (FRAGMENT).  
GN AP2.





Query Match	58.8%	Score 397;	DB 13;	Length 133;
Best Local Similarity	57.6%;	Pred. No. 4.9e-30;		
Matches	76;	Conservative 19;	Mismatches 37;	Indels 0; Gaps 0;
Qy	1	MCDAFGTGWKLVSSEFDDYMKVGVGFATPKVAGMAKPNWIIISVNGDVITIKSESTFKN	60	
Db	1			
	1	MVDVFGTWNLKOSEKFEDEYMKLGVGFATQGVGNVTKPTIIISVEGDKVTLKTQSAIKN	60	
Qy	61	TEISFIILGQEFDEVTADDRVKVSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVLVECVM	120	
Db	61			
	61	TELSFKLDEFEDETTADDRKVSFVTVDGGKLVHTQKWDGKETSILRVENGNNLTILKM	120	
Qy	121	KGVTSTRVYERA	132	
Db	121			
	121	DDVESIRRYVKA	132	

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	670	99.3	131	1	FABA_HUMAN	P15090 homo sapien
2	620	91.9	131	1	FABA_MOUSE	P04117 mus musculus
3	608	90.1	131	1	FABA_PIG	O97788 sus scrofa
4	607	89.9	131	1	FABA_RAT	P70623 rattus norv
5	573	84.9	131	1	FABA_BOVIN	P48035 bos taurus
6	482	71.4	131	1	MYP2_RABIT	P02691 oryctolagus
7	472	69.9	132	1	FABH_RAT	P07483 rattus norv
8	466	69.0	132	1	FABH_MOUSE	P11404 mus musculus
9	459	68.0	131	1	MYP2_HUMAN	P02689 homo sapien
10	448	66.4	131	1	MYP2_BOVIN	P03690 bos taurus
11	446	66.1	131	1	MYP2_MOUSE	P24526 mus musculus
12	445	65.9	132	1	FABH_HUMAN	P05413 homo sapien
13	442	65.5	132	1	FABH_BOVIN	P10790 bos taurus
14	442	65.5	132	1	FABH_PIG	Q02772 sus scrofa
15	425	63.0	131	1	FABH_BOVIN	Q09139 bos taurus
16	424	62.8	132	1	FABH_ONCMY	O13308 oncorhynchus
17	395	58.5	131	1	FABH_HUMAN	O15540 homo sapien
18	390	57.8	132	1	TLBP_RAT	P35054 rattus norv
19	388	57.5	131	1	FABH_CHICK	Q05423 gallus gall
20	386	57.2	132	1	TLBP_MOUSE	Q08716 mus musculus
21	381	56.4	131	1	FABH_RAT	P55051 rattus norv
22	378	56.0	132	1	FABL_GINCI	P80049 ginglymosto
23	377	55.9	131	1	FABB_MOUSE	P51880 mus musculus
24	367	54.4	135	1	FABE_BOVIN	P55052 bos taurus
25	366	54.2	135	1	FABE_HUMAN	Q01469 homo sapien
26	362	53.6	135	1	FABE_MOUSE	Q05816 mus musculus
27	361	53.5	135	1	FABE_RAT	P55053 rattus norv
28	326	48.3	114	1	FABL_LAMJA	P82188 lampetra jar
29	270	5	40.1	133	FABP_SCHGR	Q02970 echinococcu
30	250	37.0	131	1	FABP_SCHGR	Q095p1 lepidoglyph
31	238	35.3	130	1	FABP_LEPDS	Q17284 blomia trop
32	229.5	34.0	133	1	FABP_SCHGR	P29498 schistosoma
33	227	33.6	133	1	FABM_SCHGR	P41496 schistocerc

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Oy 2 CDAFVGTWKLVSSENFDDYKMEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNT 61
Db 1 CDAFVGTWKLVSSENFDDYKMEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNT 60
Oy 62 EISFILGQEFDEVADTKRKVKSTITLDGGVLVHVQKWDGKSTTKRKREDDKLVVECVMK 121
Db 61 EISFILGQEFDEVADTKRKVKSTITLDGGVLVHVQKWDGKSTTKRKREDDKLVVECVMK 120
Oy 122 GVTSTRVYERA 132
Db 121 GVTSTRVYERA 131
RESULT 2
FABA_MOUSE STANDARD; PRT; 131 AA.
AC P04117;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
RT Fatty acid-binding protein, adipocyte (AFABP) (Adipocyte lipid-binding
RT protein) (ALBP) (P2 adipocyte protein) (Myelin P2 protein homolog)
DE (3T3-L1 lipid binding protein) (422 protein) (P15).
GN FABP4 OR AP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84298159; PubMed=6206497;
RA Bernlohr D.A., Angus C.W., Lane M.D., Bolanowski M.A., Kelly T.J. Jr.;
RT "Expression of specific mRNAs during adipose differentiation:
RT identification of an mRNA encoding a homologue of myelin P2
RT protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5468-5472(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=8623319; PubMed=3520554;
RA Hunt C.R., Ro J.H.-S., Dobson D.E., Min H.Y., Spiegelman B.M.;
RT "Adipocyte P2 gene: developmental expression and homology of
RT 5'-flanking sequences among fat cell-specific genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:3786-3790(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86278164; PubMed=3015943;
RA Phillips M., Djian P., Green H.;
RT "The nucleotide sequence of three genes participating in the adipose
RT differentiation of 3T3 cells.";
RL J. Biol. Chem. 261:10821-10827(1986).
RN [4]
RP SEQUENCE OF 1-10 FROM N.A.
RX MEDLINE=88203618; PubMed=2452440;
RA Cook J.S., Lucas J.J., Sibley E., Bolanowski M.A., Christy R.J.,
RA Kelly T.J. Jr., Lane M.D.;
RT "Expression of the differentiation-induced gene for fatty acid-binding
RT protein is activated by glucocorticoid and cAMP.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:2949-2953(1988).
RN [5]
RP SEQUENCE.
RX MEDLINE=89008309; PubMed=2844775;
RA Matarese V., Bernlohr D.A.;
RT "Purification of murine adipocyte lipid-binding protein.
RT Characterization as a fatty acid- and retinoic acid-binding
RT protein.";
RL J. Biol. Chem. 263:14544-14551(1988).
RN [6]
RP SEQUENCE OF 10-131 FROM N.A.
RX MEDLINE=85105214; PubMed=3968175;
RA Cook K.S., Hunt C.R., Spiegelman B.M.;
RT "Developmentally regulated mRNAs in 3T3-adipocytes: analysis of
RT transcriptional control.";
RL J. Cell Biol. 100:514-520(1985).
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RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=92207973; PubMed=1554730;
RA Xu Z., Bernlohr D.A., Banaszak L.J.;
RT "Crystal structure of recombinant murine adipocyte lipid-binding
RT protein.";
RL Biochemistry 31:3484-3492(1992).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
RX MEDLINE=93216758; PubMed=8463311;
RA Xu Z., Bernlohr D.A., Banaszak L.J.;
RT "The adipocyte lipid-binding protein at 1.6-A resolution. Crystal
RT structures of the apoprotein and with bound saturated and unsaturated
RT fatty acids.";
RL J. Biol. Chem. 268:7874-7884(1993).
CC -1- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG
CC CHAIN FATTY ACID AND RETINOIC ACID.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC 'TRANSPORTERS'.
CC -----
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CC -----
CC EMBL; K02109; AAA39416.1; -
CC EMBL; M13264; AAA39870.1; -
CC EMBL; M13261; AAA39870.1; JOINED.
CC EMBL; M13262; AAA39870.1; JOINED.
CC EMBL; M13263; AAA39870.1; JOINED.
CC EMBL; M13385; AAA39417.1; -
CC EMBL; M20497; AAA37188.1; -
CC EMBL; M28726; AAA37112.1; -
CC PIR; A05089; A05089.
CC PIR; A24884; A24884.
CC PIR; A30810; A30810.
CC PIR; B25952; B25952.
CC PDB; 1ALB; 31-OCT-93.
CC PDB; 1LIB; 30-APR-94.
CC PDB; 1LIC; 30-APR-94.
CC PDB; 1LID; 30-APR-94.
CC PDB; 1LIE; 30-APR-94.
CC PDB; 1LIF; 30-APR-94.
CC PDB; 1ADL; 20-DEC-94.
CC PDB; 1AB0; 16-JUN-97.
CC PDB; 1ACD; 16-JUN-97.
CC PDB; 1A18; 01-JUL-98.
CC PDB; 1A20; 01-JUL-98.
CC SWISS-2DPAGE; P04117; MOUSE.
CC MGD; MGI:88038; Fabp4.
CC InterPro; IPR000463; Fatty_acid_BP.
CC InterPro; IPR000566; Lipocin_cytFABP.
CC Pfam; PF00061; lipocalin; 1.
CC PRINTS; PR00178; FATTVACIDBP.
CC PROSITE; PS00214; FABP; 1.
KW Transport; Lipid-binding; Phosphorylation; 3D-structure.
FT INIT_MET 0
FT MOD_RES 19 19
FT CONFLICT 39 39
FT CONFLICT 110 110
FT HELIX 2 4
FT STRAND 6 14
FT HELIX 16 23
FT TURN 24 24
FT HELIX 27 35
FT STRAND 39 45
FT TURN 46 47
FT STRAND 48 54
FT PHOSPHORYLATION (BY TYR-KINASES)
FT (BY SIMILARITY).
FT N -> T (IN REF. 2; AAA39870).
FT G -> V (IN REF. 3; AAA39417).
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FT STRAND 59 64
FT TURN 66 67
FT STRAND 70 73
FT TURN 75 76
FT STRAND 79 87
FT TURN 88 89
FT STRAND 90 97
FT TURN 98 99
FT STRAND 100 109
FT TURN 110 111
FT STRAND 112 119
FT TURN 120 121
FT STRAND 122 130
FT SEQUENCE 131 AA; ED57D4E2774B8E32 CRC64;

Query Match 91.9%; Score 620; DB 1; Length 131;
Best Local Similarity 91.6%; Pred. No. 4.3e-49;
Matches 120; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

2 CDAFVGWTKLVSSNFDDYMKVGVGFATRKVAGMKNMIIISVNGDVITIKSESTFKNT 61
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1 CDAFVGWTKLVSSNFDDYMKVGVGFATRKVAGMKNMIIISVNGDLVITIRSESTFKNT 60
|||||

62 EISFILGQEFDEVTDADRKKVKTITLDGGVLVHVQKWDGKSTTIKRRDDKLVVECVMK 121
|||||
61 EISFKLGQEFDEVTDADRKKVKTITLDGGALVQVQKWDGKSTTIKRRDGDGLVVECVMK 120
|||||

122 GVTSTRYVERA 132
|||||
121 GVTSTRYVERA 131
|||||

RESULT 3
FABA_PIG STANDARD; PRT; 131 AA.
AC O97788:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Fatty acid-binding protein, adipocyte (AFABP) (Adipocyte lipid-binding
DE protein) (ALBP) (A-FABP) (AP2).
GN FABP4.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
STRAIN-DUROC; TISSUE=Liver;
MEDLINE=9909248; PubMed=9880671;
RA Gerbens F., Jansen A., van Erp A.J.M., Harders F., Meuwissen T.H.E.,
RA Rettenberger G.F.W., Veerkamp J.H., te Pas M.F.W.;
RT "The adipocyte fatty acid-binding protein locus: characterization and
RT association with intramuscular fat content in pigs.";
RL Mamm. Genome 9:1022-1026(1998).
RN [2]
RN SEQUENCE OF 36-47, AND TISSUE SPECIFICITY.
TISSUE=Fat;
RX MEDLINE=90241143; PubMed=2334399;
RA Armstrong M.K., Bernlohr D.A., Storch J., Clarke S.D.;
RT "The purification and characterization of a fatty acid binding protein
RT specific to pig (Sus domesticus) adipose tissue.";
RL Biochem. J. 267:373-378(1990).
CC CC -1- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG
CC CHAIN FATTY ACID AND RETINOIC ACID.
CC CC -1- FUNCTION: INVOLVED IN THE REGULATION OF INTRAMUSCULAR FAT
CC ACCRETION.
CC CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC CC -1- TISSUE SPECIFICITY: ADIPOSE TISSUE.
CC CC -1- PTM: THE N-TERMINUS IS BLOCKED.
CC CC -1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CBAP FAMILY OF
CC TRANSPORTERS.

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Y16039; CAA75995.1; -.
CC HSP; P04117; ILID.
CC InterPro; IPR000463; Fatty acid_BP.
CC InterPro; IPR000566; Lipocalin_cytFABP.
CC Pfam; PF00061; lipocalin; 1.
CC PRINTS; PR00178; FATTYACIDBP.
CC PROSITE; PS00214; FABP; 1.
CC Transport; Lipid-binding; Phosphorylation.
CC INIT_MET 0 BY SIMILARITY.
CC MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)
CC FT (BY SIMILARITY).
CC SEQUENCE 131 AA; 14545 MW; 656CB0CA08CD4AB2 CRC64;

Query Match 90.1%; Score 608; DB 1; Length 131;
Best Local Similarity 88.5%; Pred. No. 5.1e-48;
Matches 116; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

2 CDAFVGWTKLVSSNFDDYMKVGVGFATRKVAGMKNMIIISVNGDVITIKSESTFKNT 61
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1 CDAFVGWTKLVSSNFDDYMKVGVGFATRKVAGMKNLIIIVNGDMITIRSESTFKNT 60
|||||

62 EISFILGQEFDEVTDADRKKVKTITLDGGVLVHVQKWDGKSTTIKRRDDKLVVECVMK 121
|||||
61 EIAFKLGQEFDEVTDADRKKVKTITLDGGALVQVQKWDGKTTTINRKIVDDKLVVECVIMK 120
|||||

122 GVTSTRYVERA 132
|||||
121 GVTSTRYVERA 131
|||||

RESULT 4
FABA_RAT STANDARD; PRT; 131 AA.
AC P70623;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Fatty acid-binding protein, adipocyte (AFABP) (Adipocyte lipid-binding
DE protein) (ALBP).
GN FABP4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A.
RA Prinsen C., Veerkamp J.H.;
RA Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC CC -1- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG
CC CHAIN FATTY ACID AND RETINOIC ACID.
CC CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC CC -1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CBAP FAMILY OF
CC TRANSPORTERS.
CC -----
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CC -----
CC EMBL; U75581; AAB18344.1; -.

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DR	PRINTS; PR00178; FATTYACIDBP.
DR	PROSITE; PS00214; FABP; 1.
KW	Transport; Lipid-binding; Phosphorylation.
FT	INIT_MET 0
FT	MOD_RES 19
FT	PHOSPHORYLATION (BY TYR-KINASES)
FT	(BY SIMILARITY).
FT	(BY SIMILARITY).
FT	SEQUENCE 131 AA; 14547 MW; A7D81B036C972D68 CRC64;
Query Match	84.9%; Score 573; DB 1; Length 131;
Best Local Similarity	84.0%; Pred. No. 7 le-45;
Matches 110; Conservative	8; Mismatches 13; Indels 0; Gaps
QY	2 CDAFVGTKLVSSNEDDYKKEVGVGFATRKVKVAGMAKPNMIISVNGDVITIKSESTFKNT 61
Db	1 CDAFVGTKLVSSNEDDYKKEVGVGFATRKVKVAGMAKPTLIISLNGGVVTKSESTFKNT 60
QY	62 EIFSILGQEFDEVTADRRKVKSTITLDGGVLVHVQKWDGKSTTIKKREDDKLWVSCVMK 121
Db	61 EIFSKLGQEFDEITPDORVKVKSIVNLDEGALVQVQNDGKSTTIKKRLMDDKRVLCVMN 120
QY	122 GVTSTRVYERA 132
Db	121 GVTATRVYERA 131
RESULT 6	
MYP2_RABIT	STANDARD; PRT; 131 AA.
AC	P02691;
DT	21-JUL-1986 (Rel. 01, Created)
DT	01-JUL-1989 (Rel. 11, Last sequence update)
DE	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Myelin P2 protein.
GN	PMP2
OS	Oryctolagus cuniculus (Rabbit).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX	NCBI_TaxID=9986;
RN	[1]
RN	SEQUENCE FROM N.A.
RX	MEDLINE=88228063; PubMed=2453513;
RX	Narayanan V., Barbosa E., Reed R., Tennekoon G.;
RT	"Characterization of a cloned cDNA encoding rabbit myelin P2
RT	protein.";
RL	J. Biol. Chem. 263:8332-8337(1988).
RL	[2]
RN	SEQUENCE OF 1-55.
RX	MEDLINE=80094496; PubMed=7356651;
RX	Ishaque A., Hofmann T., Rhee S., Eylar E.H.;
RT	"The NH2-terminal region of the P2 protein from rabbit sciatic nerve
RT	myelin.";
RL	J. Biol. Chem. 255:1058-1063(1980).
RN	[3]
RN	SEQUENCE OF 55-131.
RX	MEDLINE=82098098; PubMed=6172423;
RX	Ishaque A., Hofmann T., Eylar E.H.;
RT	"The complete amino acid sequence of the rabbit P2 protein.";
RL	J. Biol. Chem. 257:592-595(1982).
CC	-!- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
CC	CELLS.
CC	-!- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER
CC	CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN
CC	PROTEIN.
CC	-!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC	TRANSPORTERS.
CC	-----
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CC or send an email to license@isb-sib.ch).

CC -----  
DR EMBL: J03744; AAA31451.1; -  
DR PIR: A03145; MPRB2.  
DR PIR: A28081; A28081.  
DR HSP: P02690; 1PMP.  
DR InterPro: IPR000463; Fatty\_acid\_BP.  
DR InterPro: IPR000566; Lipocalin\_cycFABP.  
DR Pfam: PF00061; Lipocalin; 1.  
DR PRINTS: PR00178; FATTYACIDBP.  
DR PROSITE: PS00214; FABP; 1.  
KW Myelin; Lipid-binding; Transport; Acetylation.  
FT INIT\_MET 0 0  
FT MOD\_RES 0 1 ACETYLATION.  
FT CONFLICT 72 72 E -> Q (IN REF. 3).  
FT CONFLICT 83 83 I -> T (IN REF. 3).  
FT CONFLICT 98 98 D -> N (IN REF. 3).  
SQ SEQUENCE 131 AA; 14791 MW; E53788F693BC6A0E CRC64;  
  
Query Match 71.4%; Score 482; DB 1; Length 131;  
Best Local Similarity 72.4%; Pred. No. 1e-36;  
Matches 92; Conservative 14; Mismatches 21; Indels 0; Gaps 0;  
  
QY 5 FVGTWKLVSSENFDDYMKVGVGFATKRVAGMAKPNMIIISVNGDVITIKSETFKNTAIS 64  
DB 4 FLGTWKLVSSENFDDYMKVLGVGLATKRLGNLAKPNVLIISKGGDIITRTSETFKNTAIS 63  
QY 65 FILQGEFDEVTADRRKVKSTITLDDGVLVHVKQWKGDKSTTKRKREDDKLWVECVKMGVT 124  
DB 64 FLQGEFEETADNRKTKSIITLGRALNQVQWKGDKETIKRLVLDGKVVVECKMGVV 123  
QY 125 STRVYER 131  
DB 124 CTRIYK 130  
  
RESULT 7  
FABH\_RAT STANDARD; PRT; 132 AA.  
AC P07483;  
DT 01-APR-1988 (Rel. 07, Created)  
DT 01-AUG-1988 (Rel. 08, Last sequence update)  
DE 01-FEB-1996 (Rel. 33, Last annotation update)  
DE Fatty acid-binding protein, heart (H-FABP).  
GN FABP3.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
NCBI\_TaxID=10116;  
[1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87250640; PubMed=3036869;  
RA Heuckeroth R.O., Birkenmeier E.H., Levin M.S., Gordon J.I.;  
RT "Analysis of the tissue-specific expression, developmental  
RT regulation, and linkage relationships of a rodent gene encoding heart  
RT fatty acid binding protein.";  
RL J. Biol. Chem. 262:9709-9717(1987).  
[2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88107756; PubMed=3427112;  
RA Claffey K.P., Herrera V.L., Brecher P., Ruiz-Opazo N.;  
RT "Cloning and tissue distribution of rat heart fatty acid binding  
RT protein mRNA: identical forms in heart and skeletal muscle.";  
RL Biochemistry 26:7900-7904(1987).  
[3]  
RP SEQUENCE  
RX MEDLINE=88153733; PubMed=3162235;  
RA Gibson B.W., Yu Z., Aberth W., Burlingame A.L., Bass N.M.;  
RT "Revision of the blocked N terminus of rat heart fatty acid-binding  
RT protein by liquid secondary ion mass spectrometry.";  
RL J. Biol. Chem. 263:4182-4185(1988).  
[4]

RP PRELIMINARY SEQUENCE.  
RX MEDLINE=86250713; PubMed=2424895;  
RA Sacchetti J.C., Said B., Schulz H., Gordon J.I.;  
RT "Rat heart fatty acid-binding protein is highly homologous to the  
RT murine adipocyte 422 protein and the P2 protein of peripheral nerve  
RT myelin.";  
RL J. Biol. Chem. 261:8218-8223(1986).  
[5]  
RP SEQUENCE.  
RC TISSUE=Kidney;  
RX MEDLINE=91170283; PubMed=2005132;  
RA Kimura H., Odani S., Nishi S.-I., Sato H., Arakawa M., Ono T.;  
RT "Primary structure and cellular distribution of two fatty  
RT acid-binding proteins in adult rat kidneys.";  
RL J. Biol. Chem. 266:5963-5972(1991).  
[6]  
RP SEQUENCE OF 58-86.  
RX MEDLINE=89374061; PubMed=2775193;  
RA Kimura H., Hitomi M., Odani S., Koide T., Arakawa M., Ono T.;  
RT "Rat heart fatty acid-binding protein. Evidence that supports the  
RT amino acid sequence predicted from the cDNA.";  
RL Biochem. J. 260:303-306(1989).  
[7]  
RP PARTIAL SEQUENCE.  
RC TISSUE=Stomach;  
RX MEDLINE=90032682; PubMed=2806260;  
RA Kanda T., Iseki S., Hitomi M., Kimura H., Odani S., Kondo H.,  
RA Matsubara Y., Muto T., Ono T.;  
RT "Purification and characterization of a fatty-acid-binding protein  
RT from the gastric mucosa of rats. Possible identity with heart  
RT fatty-acid-binding protein and its parietal cell localization.";  
RL Eur. J. Biochem. 185:27-33(1989).  
[8]  
RP PARTIAL SEQUENCE.  
RC TISSUE=Mammary gland;  
RX MEDLINE=88326235; PubMed=3415652;  
RA Jones P.D., Carne A., Bass N.M., Grigor M.R.;  
RT "Isolation and characterization of fatty acid binding proteins from  
RT mammary tissue of lactating rats.";  
RL Biochem. J. 251:919-925(1988).  
[9]  
RP PARTIAL SEQUENCE.  
RC TISSUE=Mammary gland;  
RX MEDLINE=94162301; PubMed=8117746;  
RA Nielsen S.O., Rump R., Hoejrup P., Roepstorff P., Spener F.;  
RT "Differential regulation and phosphorylation of the fatty acid-  
RT binding protein from rat mammary epithelial cells.";  
RL Biochim. Biophys. Acta 1211:189-197(1994).  
CC -1- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR  
CC TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- TISSUE SPECIFICITY: HEART, BUT ALSO SKELETAL MUSCLE, KIDNEY,  
CC BRAIN AND MAMMARY GLAND.  
CC -1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPP FAMILY OF  
CC TRANSPORTERS.  
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CC -----  
DR EMBL: J02773; AAA41136.1; -  
DR PIR: A28338; A28338.  
DR PIR: A27452; A27452.  
DR PIR: A28197; A28197.  
DR PIR: A28458; A28458.  
DR PIR: A39551; A39551.  
DR PIR: S06478; S06478.  
DR HSP: P05413; 1HMT.

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DR InterPro: IPR000463; Fatty_acid_BP.
DR InterPro: IPR000566; Lipocln_cytfabp.
DR Pfam: PF00061; lipocalin; 1.
DR PRINTS: PR00178; FATTYACIDBP.
DR PROSITE: PS00214; FABP; 1.
KW Transport; Lipid-binding; Acetylation; Phosphorylation.
FT INIT_MET 0
FT MOD_RES 1 1 ACETYLATION.
FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES).
FT CONFLICT 63 63 S -> SN (IN REF. 3).
FT CONFLICT 69 69 E -> Q (IN REF. 5).
FT CONFLICT 70 70 F -> D (IN REF. 3).
SQ SEQUENCE 132 AA; 14643 MW; 31B4C6A8BFB45BE CRC64;

Query Match 69.9%; Score 472; DB 1; Length 132;
Best Local Similarity 70.5%; Pred. No. 8.2e-36;
Matches 91; Conservative 11; Mismatches 27; Indels 0; Gaps 0;

3 DAFVGTWKLVSSENFDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTE 62
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2 DAFVGTWKLVDKFNFDYMKSLGSLGVGFATQVASMTPPTIIIEKNGDTITIKTHSTFKNTE 61
||||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||

QY 63 ISFILGQEFDEVTDADRKRKSVTLTDLGVLVHVQKWDGKSTTIKRREDDKLVVCEYKMG 122
||||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
DB 62 ISFOLGVEFDEVTDADRKRKSVTLTDLGGLVHVQKWDGQETTLRELSDGKLILTLTHGN 121
||||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||

QY 123 VTSTRVYER 131
| ||| ||:
DB 122 VVSTRTYEK 130
| ||| ||:

RESULT 8
FABH_MOUSE
ID FABH_MOUSE STANDARD; PRT; 132 AA.
AC P11404;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fatty acid-binding protein, heart (H-FABP) (Mammary-derived growth
DE inhibitor) (MDGI).
GN FABP3 OR FABPH1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA;
RX MEDLINE=89296486; PubMed=2740224;
RA Tweedie S., Edwards Y.;
RT "cDNA sequence for mouse heart fatty acid binding protein, H-FABP.";
RL Nucleic Acids Res. 17:4374-4374(1989).
RN [2]
RP REVISIONS TO 2-3.
RA Tweedie S.;
RL Submitted (AUG-1989) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR SWISS; TISSUE=Liver;
RX MEDLINE=95011621; PubMed=7926807;
RA Treuner M., Kozak C.A., Gallahan D., Grosse R., Mueller T.;
RT "Cloning and characterization of the mouse gene encoding
RT mammary-derived growth inhibitor/heart-fatty acid-binding protein.";
RL Gene 147:237-242(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Mammary gland;
RX MEDLINE=93054235; PubMed=1429365;
RA Binas B., Spitzer E., Zschiesche W., Erdmann B., Kurtz A., Mueller T.,
RA Niemann C., Blenau W., Grosse R.;
RT "Hormonal induction of functional differentiation and mammary-derived
RT growth inhibitor expression in cultured mouse mammary gland

```

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RT explants.";
RL In Vitro Cell. Dev. Biol. 28A:625-634(1992).
CC -!- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR
CC TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
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CC -----
CC EMBL: X14961; CAA33084.1; -.
CC DR EMBL: U02884; AAA61933.1; -.
CC DR EMBL: U02883; AAA03445.1; -.
CC DR PIR: S04591; S04591.
CC DR HSP: P05413; IHMT.
CC DR SWISS-2DPAGE: P11404; MOUSE.
CC DR MGD; MGI:95476; Fabp3.
CC DR InterPro: IPR000463; Fatty_acid_BP.
CC DR InterPro: IPR000566; Lipocln_cytfabp.
CC DR Pfam: PF00061; lipocalin; 1.
CC DR PRINTS: PR00178; FATTYACIDBP.
CC DR PROSITE: PS00214; FABP; 1.
KW Transport; Lipid-binding; Acetylation; Phosphorylation.
FT INIT_MET 0
FT MOD_RES 1 1
FT MOD_RES 19 19 ACETYLATION (BY TYR-KINASES)
FT CONFLICT 33 33 A -> G (IN REF. 1).
FT CONFLICT 98 98 D -> N (IN REF. 3 AND 4).
FT SEQUENCE 132 AA; 14689 MW; F78BAE6DACIAB6A CRC64;

Query Match 69.0%; Score 466; DB 1; Length 132;
Best Local Similarity 69.0%; Pred. No. 2.8e-35;
Matches 89; Conservative 14; Mismatches 26; Indels 0; Gaps 0;

QY 3 DAFVGTWKLVSSENFDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTE 62
||||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
DB 2 DAFVGTWKLVDKFNFDYMKSLGSLGVGFATQVASMTPPTIIIEKNGDTITIKTHSTFKNTE 61
||||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||

QY 63 ISFILGQEFDEVTDADRKRKSVTLTDLGVLVHVQKWDGKSTTIKRREDDKLVVCEYKMG 122
||||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
DB 62 ISFOLGIEFDEVTDADRKRKSVTLTDLGGLVHVQKWDGQETTLRELVDGKLILTLTHGS 121
||||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||

QY 123 VTSTRVYER 131
| ||| ||:
DB 122 VVSTRTYEK 130
| ||| ||:

RESULT 9
MYP2_HUMAN
ID MYP2_HUMAN STANDARD; PRT; 131 AA.
AC P02689;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myelin P2 protein.
GN PMP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92068191; PubMed=1720307;
RA Hayaoka K., Nanao K., Tahara M., Sato W., Takada G., Miura M.,
RA Uyemura K.;

```



RT "Isolation and sequence determination of cDNA encoding P2 protein of  
 RL human peripheral myelin.";  
 RN Biochem. Biophys. Res. Commun. 181:204-207(1991).  
 RP [2]  
 RX MEDLINE=83058785; PubMed=6183401;  
 RA Suzuki M., Kitamura K., Sakamoto Y., Uyemura K.;  
 RT "The complete amino acid sequence of human P2 protein.";  
 RL J. Neurochem. 39:1759-1762(1982).  
 RN [3]  
 RP SEQUENCE OF 1-115 FROM N.A.  
 RX MEDLINE=95054012; PubMed=7525873;  
 RA Narayanan V., Ripepi B., Jabs E.W., Hawkins A., Griffin C.,  
 RT Tennekoon G.;  
 RA "Partial structure and mapping of the human myelin P2 protein gene.";  
 RL J. Neurochem. 63:2010-2013(1994).  
 RN [1]  
 RP FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN  
 CC CELLS.  
 CC -|- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER  
 CC CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN  
 CC PROTEIN.  
 CC -|- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF  
 CC TRANSPORTERS.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; D16181; BAA03726.1; -;  
 DR EMBL; D16179; BAA03726.1; JOINED.  
 DR EMBL; D16180; BAA03726.1; JOINED.  
 DR EMBL; X62167; CAA44096.1; -;  
 DR EMBL; S73470; AAB32592.2; -;  
 DR EMBL; S73468; AAB32592.2; JOINED.  
 DR EMBL; S73469; AAB32592.2; JOINED.  
 DR PIR; A03143; MPB02.  
 DR PIR; JT0977; JT0977.  
 DR HSSP; P02690; 1PMP.  
 DR MIN; 170715; -;  
 DR InterPro; IPR000463; Fatty\_acid\_BP.  
 DR InterPro; IPR000566; Lipocln\_cytfabp.  
 DR Pfam; PF00061; lipocalin; 1.  
 DR PRINTS; PR00178; FATTYACIDBP.  
 DR PROSITE; PS00214; FABP; 1.  
 DR Myelin; Lipid-binding; Transport; Acetylation.  
 DR INIT\_MET 0 0  
 DR MOD\_RES 1 1 ACETYLATION.  
 DR DISULFID 117 124  
 FT CONFLICT 24 24 G -> GG (IN REF. 3).  
 FT CONFLICT 98 98 D -> N (IN REF. 2).  
 FT CONFLICT 110 110 N -> D (IN REF. 2).  
 SQ SEQUENCE 131 AA; 14778 MW; 3D0E640BA03E69D2 CRC64;

Query Match 68.0%; Score 459; DB 1; Length 131;  
 Best Local Similarity 68.5%; Pred. No. 1.2e-34;  
 Matches 87; Conservative 16; Mismatches 24; Indels 0; Gaps 0;

QY 5 FVGTWKLVSSNFDDYMKVEGVGFATRKVAGMAKPMIISVNGDVITIKSESTFKNTEIS 64  
 DB 4 FLGTWKLVSSNFDDYMKALGVGLATRKLGNAKPTVIAISKKGDIITITESTFKNTEIS 63  
 QY 65 FTLQGEFEVTDADRRKVKSTITLDGGLVHVOKWQDGKSTTIKRRDDKLVLVVECVMKGYT 124  
 DB 64 FKLQGEFEETADNRKTKSTVTLQKSLNQVQWQDGKSTTIKRRKLVLVNGKVAECMKGVV 123

QY 125 STRVYER 131  
 DB 124 CTRIYEK 130

RESULT 10  
 MYP2\_BOVIN  
 ID MYP2\_BOVIN STANDARD; PRT; 131 AA.  
 AC P02690;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Myelin P2 protein.  
 GN PMP2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=80225120; PubMed=6156092;  
 RA Kitamura K., Suzuki M., Suzuki A., Uyemura K.;  
 RT "The complete amino acid sequence of the P2 protein in bovine  
 RT peripheral nerve myelin.";  
 RL FEBS Lett. 115:27-30(1980).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).  
 RX MEDLINE=89005045; PubMed=2458918;  
 RA Jones T.A., Bergfors T., Sedzik J., Unge T.;  
 RT "The three-dimensional structure of P2 myelin protein.";  
 RL EMBO J. 7:1597-1604(1988).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).  
 RX MEDLINE=93253782; PubMed=7683727;  
 RA Cowan S.W., Newcomer M.E., Jones T.A.;  
 RT "Crystallographic studies on a family of cellular lipophilic  
 RT transport proteins. Refinement of P2 myelin protein and the structure  
 RT determination and refinement of cellular retinol-binding protein in  
 RT complex with all-trans-retinol.";  
 RL J. Mol. Biol. 230:1225-1246(1993).  
 CC -|- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN  
 CC CELLS.  
 CC -|- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER  
 CC CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN  
 CC PROTEIN.  
 CC -|- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF  
 CC TRANSPORTERS.  
 DR PIR; A03144; MPB02.  
 DR PDB; 1PMP; 26-JAN-95.  
 DR InterPro; IPR000463; Fatty\_acid\_BP.  
 DR InterPro; IPR000566; Lipocln\_cytfabp.  
 DR Pfam; PF00061; lipocalin; 1.  
 DR PRINTS; PR00178; FATTYACIDBP.  
 DR PROSITE; PS00214; FABP; 1.  
 DR Myelin; Lipid-binding; Transport; Acetylation; 3D-structure.  
 FT MOD\_RES 1 1 ACETYLATION.  
 FT DISULFID 117 124  
 SQ SEQUENCE 131 AA; 14818 MW; 1424AAF386EA0B21 CRC64;

Query Match 66.4%; Score 448; DB 1; Length 131;  
 Best Local Similarity 67.7%; Pred. No. 1.2e-33;  
 Matches 86; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

QY 5 FVGTWKLVSSNFDDYMKVEGVGFATRKVAGMAKPMIISVNGDVITIKSESTFKNTEIS 64  
 DB 4 FLGTWKLVSSNFDDYMKALGVGLATRKLGNAKPTVIAISKKGDIITITESTFKNTEIS 63  
 QY 65 FTLQGEFEVTDADRRKVKSTITLDGGLVHVOKWQDGKSTTIKRRDDKLVLVVECVMKGYT 124  
 DB 64 FKLQGEFEETADNRKTKSTVTLQKSLNQVQWQDGKSTTIKRRKLVLVNGKVAECMKGVV 123

QY 125 STRVYER 131  
 DB 124 CTRIYEK 130

```
RESULT 11
MYP2_MOUSE STANDARD; PRT; 131 AA.
ID MYP2_MOUSE
AC P24526;
DT 01-MAR-1992 (Rel. 21, Created)
DE 01-MAR-1992 (Rel. 21, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myelin P2 protein.
GN PMP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=9126811; PubMed=1711100;
RA Narayanan V., Kaestner K.H., Tennekoon G.I.;
RT "Structure of the mouse myelin P2 protein gene.";
RL J. Neurochem. 57:75-80(1991).
CC -1- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
CC CELLS.
CC -1- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER
CC CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN
CC PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPP FAMILY OF
CC TRANSPORTERS.
CC -----
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CC -----
DR EMBL; S39508; AAB19249.2; -
DR PIR; JH0407; JH0407.
DR HSSP; P02690; 1PMP.
DR MGP; MGI:102667; Pmp2.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipoclin_cytFABP.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Myelin; Lipid-binding; Transport; Acetylation.
FT INIT_MET 0 0 BY SIMILARITY.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
SQ SEQUENCE 131 AA; 14804 MW; AB357746F152E07C CRC64;

Query Match 66.18; Score 446; DB 1; Length 131;
Best Local Similarity 66.18; Pred. No. 1.7e-33;
Matches 84; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

Qy 5 FVGTWKLVSSENFDDYMKVEGVGFKTRKVGAKMPNMIISVNGDVITIKSESTFKNTEIS 64
I:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Dy 4 FLGTWKLVSSENFDDYMKALGVGLNKLGNLAKPTVIISKKGDIYITIRTESAFKNTEIS 63

Qy 65 FILGQEFDEVTDARRKVKSTTLTGGVLVHVQKWDGKSTTKRKREDKLVVCEVMKGV 124
I:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Dy 64 FKLQGFEDTADNRKAKSVITLGRSLQVQKWDGKETAIRRTLLDGRMVVECIKMGW 123

Qy 125 STRVYER 131
I:||||:
Dy 124 CTRIYEK 130

RESULT 12
FABH_HUMAN STANDARD; PRT; 132 AA.
ID FABH_HUMAN
AC P05413; Q99957;
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DT 01-NOV-1988 (Rel. 09, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Fatty acid-binding protein, heart (H-FABP) (Muscle fatty acid-binding
DE protein) (M-FABP) (Mammary-derived growth inhibitor) (MDGI).
GN FABP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RX TISSUE=Skeletal muscle;
RX MEDLINE=91248148; PubMed=1710107;
RA Peeter R.A., Veerkamp J.H., Kanda T., Ono T., Geurts van Kessel A.;
RT "Cloning of the cDNA encoding human skeletal-muscle
RT fatty-acid-binding protein, its peptide sequence and chromosomal
RT localization.";
RL Biochem. J. 276:203-207(1991).
RN [2]
SEQUENCE FROM N.A.
RX TISSUE=Breast;
RA Hu Y.F., Ao X., Russo I.H., Russo J.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE FROM N.A.
RA Wu X., Arlt M., Goodfellow P.J., Rottman J.N.;
RT "Genomic organization and complete nucleotide sequence of the human
RT cardiac fatty acid binding protein gene (FABP3), and identification of
RT a closely related genomic sequence.";
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RN [4]
SEQUENCE.
RX MEDLINE=88339792; PubMed=3421901;
RA Offner G.D., Brecher P., Sawilovich W.B., Costello C.E., Troxler R.F.;
RT "Characterization and amino acid sequence of a fatty acid-binding
RT protein from human heart.";
RL Biochem. J. 252:191-198(1988).
RN [5]
REVIEWS, AND SEQUENCE.
RX MEDLINE=91094793; PubMed=2266954;
RA Boerchers T., Hoejrup P., Nielsen S.U., Roepstorff P., Spener F.,
RA Knudsen J.;
RT "Revision of the amino acid sequence of human heart fatty
RT acid-binding protein.";
RL Mol. Cell. Biochem. 98:127-133(1990).
RN [6]
SEQUENCE OF 14-132 FROM N.A.
RX TISSUE=Heart;
RX MEDLINE=94085953; PubMed=8262516;
RA Troxler R.F., Offner G.D., Jiang J.W., Wu B.L., Skare J.C.,
RA Milunsky A., Wyandt H.E.;
RT "Localization of the gene for human heart fatty acid binding protein
RT to chromosome 1p32-1p33.";
RL Hum. Genet. 92:563-566(1993).
RN [7]
SEQUENCE OF 31-38.
RX TISSUE=Heart;
RX MEDLINE=96007936; PubMed=7498159;
RA Kovalyov L.I., Shishkin S.S., Efimochkin A.S., Kovalyova M.A.,
RA Ershova E.S., Egorov T.A., Musalyamov A.K.;
RT "The major protein expression profile and two-dimensional protein
RT database of human heart.";
RL Electrophoresis 16:1160-1169(1995).
RN [8]
X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX MEDLINE=92406763; PubMed=1526991;
RA Zanotti G., Scapin G., Spadon P., Veerkamp J.H., Sacchettini J.C.;
RT "Three-dimensional structure of recombinant human muscle fatty acid-
RT binding protein.";
RL J. Biol. Chem. 267:18541-18550(1992).
RN [9]
X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS).
```



\*Purification and characterisation of a polymorphic low M(r) bovine muscle cysteine proteinase inhibitor: structural identity with fatty-acid-binding proteins.\*;  
Biochimie 75:937-945(1993).

[6]

VARIANT IN POSITION 98.

MEDLINE-9335876; PubMed-8354262;

Bartetzko N., Lezius A.G., Spener F.;

"Isoforms of fatty-acid-binding protein in bovine heart are coded by

distinct mRNA.";

Eur. J. Biochem. 215:555-559(1993).

[7]

X-RAY CRYSTALLOGRAPHY.

MEDLINE-91301134; PubMed-2070787;

Mueller-Fahrnow A., Egner U., Jones T.A., Ruedel H., Spener F.,

Saenger W.;

"Three-dimensional structure of fatty-acid-binding protein from

bovine heart.";

Eur. J. Biochem. 199:271-276(1991).

[8]

STRUCTURE BY NMR.

MEDLINE-93130916; PubMed-1483473;

Luecke C., Lassen D., Kretenkamp H.-J., Spener F., Rueterjans H.;

"Sequence-specific 1H-NMR assignment and determination of the

secondary structure of bovine heart fatty-acid-binding protein.";

Eur. J. Biochem. 210:901-910(1992).

[9]

STRUCTURE BY NMR.

MEDLINE-95324534; PubMed-7601110;

Lassen D., Luecke C., Kveder M., Mesgarzadeh A., Schmidt J.M.,

Specht B., Lezius A., Spener F., Rueterjans H.;

"Three-dimensional structure of bovine heart fatty-acid-binding

protein with bound palmitic acid, determined by multidimensional NMR

spectroscopy.";

Eur. J. Biochem. 230:266-280(1995).

[10]

STRUCTURE BY NMR.

MEDLINE-98149696; PubMed-9490052;

Mesgarzadeh A., Pfeiffer S., Engelke J., Lassen D., Rueterjans H.;

"Bound water in apo and holo bovine heart fatty-acid-binding protein

determined by heteronuclear NMR spectroscopy.";

Eur. J. Biochem. 251:781-786(1998)

-1- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR

TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.

-1- FUNCTION: MDGI REVERSIBLY INHIBITS PROLIFERATION OF MAMMARY

CARCINOMA CELLS.

-1- SUBCELLULAR LOCATION: CYTOPLASMIC OR MITOCHONDRIAL MATRIX.

-1- TISSUE SPECIFICITY: MAMMARY EPITHELIAL CELLS OF DEVELOPING

LOBULOALVEOLAR STRUCTURES AND HEART.

-1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF

TRANSPORTERS.

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EMBL; X12710; CAA31212.1; -;

EMBL; X51933; CAA36199.1; -;

PIR; A29466; A29466.

PIR; S01133; S01133.

PIR; A34676; A34676.

PIR; A37883; A37883.

PDB; 1BWY; 07-OCT-98.

InterPro; IPR000463; Fatty\_acid\_BP.

InterPro; IPR000566; Lipocln\_cytFABP.

Pfam; PF00061; Lipocalin; 1.

PRINTS; PR00178; FATTYACIDBP.

PROSITE; PS00214; FABP; 1.

Transport; Lipid-binding; Acetylation; Phosphorylation; 3D-structure.

KW

FT INIT\_MET 0 0  
FT MOD\_RES 1 1  
FT MOD\_RES 19 19  
FT MOD\_RES 19 19  
FT VARIANT 98 98  
FT CONFLICT 12 14  
FT CONFLICT 40 40  
FT CONFLICT 43 43  
FT CONFLICT 93 93  
FT CONFLICT 127 127  
SQ SEQUENCE 132 AA; 14648 MW; C6204932C6DFD35 CRC64;

Query Match 65.5%; Score 442; DB 1; Length 132;

Best Local Similarity 65.1%; Pred. No. 4e-33;

Matches 84; Conservative 15; Mismatches 30; Indels 0; Gaps 0;

Qy 3 DAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTE 62

Db 2 DAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTE 61

Qy 63 ISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKRRDDDKLVVECVMKG 122

Db 62 ISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKRRDDDKLVVECVMKG 121

Qy 123 VTSTRYER 131

Db 122 AVCRTYEK 130

RESULT 14

FABH\_PIG

ID FABH\_PIG STANDARD; PRT; 132 AA.

AC 002772;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Fatty acid-binding protein, heart (H-FABP).

GN FABP3.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

OC NCBI\_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Blood;

RX MEDLINE=97262098; PubMed=9107676;

RA Gerbens F.N.A., Rettenberger G., Lenstra J.A., Veerkamp J.H.,

Te Pas M.F.W.;

RT "Characterization, chromosomal localization, and genetic variation of

the porcine heart fatty acid-binding protein gene.";

RL Mamm. Genome 8:328-332(1997).

CC -1- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR

TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF

TRANSPORTERS.

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EMBL; X98558; CAA67168.1; -;

DR HSSP; P10790; LBWY.

DR InterPro; IPR000463; Fatty\_acid\_BP.

DR InterPro; IPR000566; Lipocln\_cytFABP.

DR Pfam; PF00061; Lipocalin; 1.

DR PRINTS; PR00178; FATTYACIDBP.

DR PROSITE; PS00214; FABP; 1.

DR PROSITE; PS00214; FABP; 1.

KW Transport; Lipid-binding; Acetylation; Phosphorylation.  
 FT INIT\_MET 0 0 BY SIMILARITY.  
 FT MOD\_RES 1 1 ACETYLATION (BY SIMILARITY).  
 FT MOD\_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES) (BY  
 FT SIMILARITY).  
 SQ SEQUENCE 132 AA; 14618 MW; B5431E65EF596C95 CRC64;

Query Match 65.5%; Score 442; DB 1; Length 132;  
 Best Local Similarity 65.1%; Pred. No. 4e-33;  
 Matches 84; Conservative 15; Mismatches 30; Indels 0; Gaps 0;

QY 3 DAFVGTWKLVSSENFDDYMKVGVGFEATRKVAGNAKPNMIIISVNGDVITIKSESTFKNTE 62  
 DB 2 DAFAGTWKLVDSKNFDDYMKSGVGFATQVANNKPTTIIIEVNGDTIIIKTQSTFKSTE 61

QY 63 ISFILGQEFDEVTADDRKVKSTITLDGVLVHVOKWKGKSTTIKRRKDDDKLVVECVKMG 122  
 DB 62 ISFKLGVEFDETTADDRKVKSTIVTLGGKLVHLQKWNGOETTLVRELVDGKLIILTLTHGS 121

123 VTSTRVYER 131  
 122 AVCTRTYEK 130

RESULT 15  
 FABB\_BOVIN  
 ID FABB\_BOVIN STANDARD; PRT; 131 AA.  
 AC Q09139;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Fatty acid-binding protein, brain (B-FABP).  
 GN FABP7.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=91094811; PubMed=2266968;  
 RA Schoentgen F., Bonanno L.M., Pignede G., Jolles P.;  
 RT "Amino acid sequence and some ligand binding properties of fatty  
 RT acid-binding protein from bovine brain.";  
 RL Mol. Cell. Biochem. 98:35-39(1990).  
 RN [2]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=90032683; PubMed=2806261;  
 RA Schoentgen F., Pignede G., Bonanno L.M., Jolles P.;  
 RT "Fatty-acid-binding protein from bovine brain. Amino acid sequence  
 RT and some properties.";  
 RL Eur. J. Biochem. 185:35-40(1989).  
 CC -1- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR  
 CC TRANSPORT OF LONG CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.  
 CC BINDS OLEIC AND PALMITIC ACIDS BUT NOT PALMITOYL COA.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF  
 CC TRANSPORTERS.  
 DR HSPSP; P10790; IBWY.  
 DR InterPro; IPR000463; Fatty\_acid\_BP.  
 DR InterPro; IPR000566; Lipocln\_cytFABP.  
 DR Pfam; PF00061; lipocalin; 1.  
 DR PRINTS; PR00178; FATTVACIDBP.  
 DR PROSITE; PS00214; FABP; 1.  
 KW Transport; Lipid-binding.  
 FT VARIANT 11 12 TE -> VD.  
 FT VARIANT 14 14 Q -> K.  
 FT VARIANT 18 18 E -> D.  
 FT VARIANT 33 34 GN -> AS.

FT VARIANT 40 40 L -> T.  
 FT VARIANT 43 44 SV -> EK.  
 FT VARIANT 49 49 E -> V.  
 FT VARIANT 65 65 H -> K.  
 FT VARIANT 68 68 E -> V.  
 FT VARIANT 72 72 D -> E.  
 FT VARIANT 78 78 Q -> R.  
 FT VARIANT 83 83 I -> V.  
 FT VARIANT 105 105 V -> T.  
 FT VARIANT 108 108 M -> L.  
 FT VARIANT 121 122 DV -> TA.  
 FT VARIANT 127 127 H -> T.  
 SQ SEQUENCE 131 AA; 14590 MW; A26FF5D63C0CF2B4 CRC64;

Query Match 63.0%; Score 425; DB 1; Length 131;  
 Best Local Similarity 62.0%; Pred. No. 1.3e-31;  
 Matches 80; Conservative 20; Mismatches 29; Indels 0; Gaps 0;

QY 3 DAFVGTWKLVSSENFDDYMKVGVGFEATRKVAGNAKPNMIIISVNGDVITIKSESTFKNTE 62  
 DB 2 DAFVGTWKLTESQNFDEYMKSLGVGFATQVGNMTKPTLIISVNGDTIIRKTSFKNTE 61

QY 63 ISFILGQEFDEVTADDRKVKSTITLDGVLVHVOKWKGKSTTIKRRKDDDKLVVECVKMG 122  
 DB 62 ISFHLGSEFDDTTADDDQKVSIVTLGGKLVHVOKWQGESLVREMGAKLIILTLTHGD 121

QY 123 VTSTRVYER 131  
 DB 122 VVAVRHYEK 130

Search completed: June 7, 2002, 18:23:20  
 Job time: 211 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 7, 2002, 18:17:38 ; Search time 16.41 Seconds  
(without alignments)  
772.931 Million cell updates/sec

Title: US-09-503-596-4  
Perfect score: 675  
Sequence: 1 MCDAFVGTWKLVSSENFDDY.....KLVECVMGVSTRYVERA 132

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	675	100.0	132	1 FZHUF	fatty acid-binding
2	623	92.3	132	2 B25952	myelin P2 protein
3	578	85.6	132	2 S57744	adipocyte-type fat
4	486	72.0	132	1 MPRB2	myelin P2 protein
5	477	70.7	133	2 A27452	fatty acid-binding
6	466	69.0	133	2 PC4011	fatty acid-binding
7	463	68.6	132	1 MPRU2	myelin P2 protein
8	450	66.7	132	2 JH0407	myelin P2 protein
9	449	66.5	133	1 F2HUC	fatty acid-binding
10	448	66.4	131	1 MPRB2	myelin P2 protein
11	446	66.1	133	2 A34676	fatty acid-binding
12	425	63.0	131	2 S06479	fatty acid-binding
13	392	58.1	132	2 A49184	fatty acid-binding
14	390	57.8	132	2 I52524	testis lipid bindi
15	385	57.0	132	2 I56510	fatty acid-binding
16	381	56.4	132	2 I58161	lipid-binding prot
17	381	56.4	132	2 I48923	fatty acid-binding
18	378	56.0	132	2 S20297	fatty acid-binding
19	366	54.2	135	2 I56326	fatty acid-binding
20	362	53.6	135	2 A47497	lipid-binding prot
21	361	53.5	135	2 JC2201	fatty acid-binding
22	307.5	45.6	135	2 T15205	hypothetical prote
23	300.5	44.5	136	2 T15207	hypothetical prote
24	286.5	38.0	137	2 T25123	hypothetical prote
25	242.5	35.9	133	2 A48578	fatty acid-binding
26	231.5	34.3	134	2 S29600	fatty acid-binding
27	229.5	34.0	133	2 A39818	14K fatty acid-bin
28	227	33.6	133	2 A44870	fatty acid-binding
29	227	33.6	134	2 S34717	retinol-binding pr

30	225	33.3	134	2 A29065	retinol-binding pr
31	223	33.0	134	2 S45378	cellular retinol b
32	223	33.0	134	2 S43470	fatty acid-binding
33	222	32.9	137	1 RJHU1	retinoic acid-bind
34	220	32.6	137	1 RJBOA	retinoic acid-bind
35	220	32.6	137	2 A35825	retinoic acid-bind
36	218	32.3	135	1 RJRTO	retinol-binding pr
37	212	31.4	135	1 RJHU0	retinol-binding pr
38	212	31.4	135	2 S16355	retinol-binding pr
39	206	30.5	134	2 S69360	retinoic acid-bind
40	203.5	30.1	138	2 A42495	retinoic acid-bind
41	201.5	29.9	138	1 RJHU2	retinoic acid-bind
42	197.5	29.3	138	2 I51265	xCRABP - African c
43	196	29.0	139	2 I53298	cellular retinoic
44	191	28.3	95	2 A61629	retinoic acid-bind
45	190	28.1	132	1 FZHUI	fatty acid-binding

ALIGNMENTS

RESULT 1

FZHUF  
fatty acid-binding protein, adipocyte - human  
N:Alternate names: adipocyte lipid-binding protein (ALBP); fatty acid binding protein  
C:Species: Homo sapiens (man)  
C:Date: 20-Dec-1989 #sequence\_revision 03-May-1996 #text\_change 22-Jun-1999  
C:Accession: A33363  
R:Baxa, C.A.; Sha, R.S.; Buelt, M.K.; Smith, A.J.; Matarese, V.; Chinander, L.L.; Bou  
Biochemistry 28, 8683-8690, 1989  
A:Title: Human adipocyte lipid-binding protein: purification of the protein and cloni  
A:Reference number: A33363; MUID: 90105597  
A:Accession: A33363  
A:Molecule type: mRNA  
A:Residues: 1-132 <BAX>  
A:Cross-references: GB:J02874; NID:gl78346; PIDN:AAA51689.1; PID:gl78347  
A:Experimental source: subcutaneous fat  
C:Genetics:  
A:Gene: GDB:FABP4  
A:Cross-references: GDB:128030  
A:Map position: lp33-1p32  
C:Superfamily: myelin P2 protein  
C:Keywords: blocked amino end; lipid binding; phosphoprotein  
F:2/Modified site: blocked amino end (Cys) (in mature form) (probably acetylated) #st  
F:20/Binding site: phosphate (Tyr) (covalent) #status predicted  
F:127,129/Binding site: fatty acid (Arg, Tyr) #status predicted

Query Match 100.0%; Score 675; DB 1; Length 132;  
Best Local Similarity 100.0%; Pred. No. 8.3e-55;  
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCDAFVGTWKLVSSENFDDYMKVEGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60

Db 1 MCDAFVGTWKLVSSENFDDYMKVEGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60

Qy 61 TEISILGQEFDEVYADRRKVKSTITLDGGVLHVQKWDGCKSTTTIKRREDKLVVEVCYM 120

Db 61 TEISILGQEFDEVYADRRKVKSTITLDGGVLHVQKWDGCKSTTTIKRREDKLVVEVCYM 120

Qy 121 KGVTSRTRYERA 132

Db 121 KGVTSRTRYERA 132

RESULT 2

B25952  
myelin P2 protein homolog - mouse  
N:Alternate names: adipocyte lipid-binding protein; adipocyte P2 protein  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 31-Dec-2000  
C:Accession: B25952; PC1249; A24884; A05089; A30810; I49440; I49467  
R:Phillips, M.; Djian, P.; Green, H.

J. Biol. Chem. 261, 10821-10827, 1986  
A:Title: The nucleotide sequence of three genes participating in the adipose differentiation  
A:Reference number: A92553; MUID:86278164  
A:Accession: B25952  
A:Molecule type: DNA  
A:Residues: 1-132 <PHI>  
A:Cross-references: GB:M13385; NID:g198718; PIDN:AAA39417.1; PID:g387401  
A:Note: the authors translated the codon GTG for residue 111 as Gly  
R:Bansal, M.P.; Medina, D.  
Biochem. Biophys. Res. Commun. 191, 61-69, 1993  
A:Title: Expression of fatty acid-binding proteins in the developing mouse mammary gland  
A:Reference number: PC1248; MUID:93191717  
A:Accession: PC1249  
A:Molecule type: protein  
A:Residues: 25-35; 37-51; 59-88 <BAN>  
A:Experimental source: mammary gland  
R:Hunt, C.R.; Ro, J.H.S.; Dobson, D.E.; Min, H.Y.; Spiegelman, B.M.  
Proc. Natl. Acad. Sci. U.S.A. 83, 3786-3790, 1986  
A:Title: Adipocyte P2 gene: Developmental expression and homology of 5'-flanking sequence  
A:Reference number: A24884; MUID:86233319  
A:Accession: A24884  
A:Molecule type: DNA  
A:Residues: 1-39, 'T', 41-110, 'G', 112-132 <HUN>  
A:Cross-references: GB:M13264; NID:g200183; PIDN:AAA39870.1; PID:g387504  
A:Note: the authors translated the codon ACC for residue 40 as Ser  
R:Bernlohr, D.A.; Angus, C.W.; Lane, M.D.; Bolanowski, M.A.; Kelly Jr., T.J.  
Proc. Natl. Acad. Sci. U.S.A. 81, 5468-5472, 1984  
A:Title: Expression of specific mRNAs during adipose differentiation: identification of  
A:Reference number: A05089; MUID:84298159  
A:Accession: A05089  
A:Molecule type: mRNA  
A:Residues: 1-110, 'G', 112-132 <BER>  
A:Cross-references: GB:R02109; NID:g198716; PIDN:AAA39416.1; PID:g293695  
R:Matrese, V.; Bernlohr, D.A.  
J. Biol. Chem. 263, 14544-14551, 1988  
A:Title: Purification of murine adipocyte lipid-binding protein. Characterization as a  
A:Reference number: A30810; MUID:89008309  
A:Accession: A30810  
A:Molecule type: protein  
A:Residues: 2-110, 'G', 112-132 <MAT>  
R:Cook, K.S.; Hunt, C.R.; Spiegelman, B.M.  
J. Cell Biol. 100, 514-520, 1985  
A:Title: Developmentally regulated mRNAs in 3T3-adipocytes: Analysis of transcriptional  
A:Reference number: I49440; MUID:85105214  
A:Accession: I49440  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 11-110, 'G', 112-132 <RES>  
A:Cross-references: GB:M28726; NID:g191492; PIDN:AAA37112.1; PID:g191493  
R:Cook, J.S.; Lucas, J.J.; Sibley, E.; Bolanowski, M.A.; Christy, R.J.; Kelly, T.J.; Lan  
Proc. Natl. Acad. Sci. U.S.A. 85, 2949-2953, 1988  
A:Title: Expression of the differentiation-induced gene for fatty acid-binding protein  
A:Reference number: I49467; MUID:88203618  
A:Accession: I49467  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-11 <RE2>  
A:Cross-references: GB:M20497; NID:g191743; PIDN:AAA37188.1; PID:g191744  
A:Experimental source: 3T3-L1 cells  
C:Genetics:  
A:Introns: 25/1; 82/3; 116/3  
C:Superfamily: myelin P2 protein  
C;Keywords: lipid binding; phosphoprotein  
Query Match 92.38; Score 623; DB 2; Length 132;  
Best Local Similarity 91.78; Pred. No. 4.8e-50;  
Matches 121; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60  
Db 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDLVITIRSESTFKN 60

Qy 61 TEISFILGOEFDEVTADDRKVKSTITLDGVLVHVQKWDGKSTTIKRRKDDKLVECVN 120  
Db 61 TEISFKLGVFEDEITADDRKVKSIITLDGALVQVKWDGKSTTIKRRKRDVDKLVECVN 120  
Qy 121 KGVTSRTRYERA 132  
Db 121 KGVTSRTRYERA 132  
RESULT 3  
S57744  
adipocyte-type fatty acid binding protein - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 19-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 13-Aug-1999  
C:Accession: S57744  
R:Specht, B.; Bartetzko, N.; Kuhl, H.; Franke, R.; Boerchers, T.; Spener, F.  
Submitted to the EMBL Data Library, June 1995  
A:Description: Mammary derived growth inhibitor - not a distinct protein but a mix of  
A:Reference number: S57744  
A:Accession: S57744  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-132 <SPE>  
A:Cross-references: EMBL:X89244; NID:g895753; PIDN:CAA61532.1; PID:g895754  
C:Superfamily: myelin P2 protein

Query Match 85.68; Score 578; DB 2; Length 132;  
Best Local Similarity 84.18; Pred. No. 6.4e-46;  
Matches 111; Conservative 8; Mismatches 13; Indels 0; Gaps 0;  
Qy 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60  
Db 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPTLIISLNGGVVVIKSESTFKN 60  
Qy 61 TEISFILGOEFDEVTADDRKVKSTITLDGVLVHVQKWDGKSTTIKRRKDDKLVECVN 120  
Db 61 TEISFKLGVFEDEITPDDRKVKSIIVNLDEGALVQVQNWGKSTTIKRRKMDKMLVECVN 120  
Qy 121 KGVTSRTRYERA 132  
Db 121 KGVTSRTRYERA 132

RESULT 4  
MPR2  
myelin P2 protein - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 30-Jun-1980 #sequence\_revision 10-May-1996 #text\_change 22-Jun-1999  
C:Accession: A28081; A92266; A92372; A03145  
R:Narayanan, V.; Barbosa, E.; Reed, R.; Tennekoon, G.  
J. Biol. Chem. 263, 8332-8337, 1988  
A:Title: Characterization of a cloned cDNA encoding rabbit myelin P-2 protein.  
A:Reference number: A28081; MUID:88228063  
A:Accession: A28081  
A:Molecule type: mRNA  
A:Residues: 1-132 <NAR>  
A:Cross-references: GB:J03744; NID:g165657; PIDN:AAA31451.1; PID:g165658  
A:Note: translation of Initiator Met is not shown  
R:Ishaque, A.; Hofmann, T.; Rhee, S.; Eylar, E.H.  
J. Biol. Chem. 255, 1058-1063, 1980  
A:Title: The NH-2-terminal region of the P2 protein from rabbit sciatic nerve myelin.  
A:Reference number: A92266; MUID:80094496  
A:Accession: A92266  
A:Molecule type: protein  
A:Residues: 2-56 <ISI>  
R:Ishaque, A.; Hofmann, T.; Eylar, E.H.  
J. Biol. Chem. 257, 592-595, 1982  
A:Title: The complete amino acid sequence of the rabbit P2 protein.  
A:Reference number: A92372; MUID:82098098  
A:Accession: A92372  
A:Molecule type: protein  
A:Residues: 56-72, 'Q', 74-83, 'T', 85-98, 'N', 100-132 <ISI>



C:Comment: p2 protein and myelin basic protein together constitute a major fraction of p2 protein  
C:Superfamily: myelin p2 protein  
C:Keywords: acetylated amino end; myelin; phosphoprotein  
F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental  
F:20/Binding site: phosphate (Tyr) (covalent) #status predicted  
F:118-125/Disulfide bonds: #status predicted

Query Match 72.0%; Score 486; DB 1; Length 132;  
Best Local Similarity 71.0%; Pred. No. 1.7e-37;  
Matches 93; Conservative 15; Mismatches 23; Indels 0; Gaps 0;  
QY 1 MCDAFVGTWKLVSSENFDDYKVGVPATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60  
DB 1 MSNFKLGTWKLVSSENFDDYKMGVLGATRKGLNGLAKPNVVISKGGDIITIRTESTFKN 60  
QY 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKKRREDDKLWVECMV 120  
DB 61 TEISFKLGQEFDEVTADNRKTKSTITLRLGALNQVQKWDGKETTIRKRLVDGKMWVECKM 120  
QY 121 KGVVSTRVYER 131  
DB 121 KGVVCTRIYK 131

RESULT 5  
A27452  
fatty acid-binding protein - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 13-Aug-1999  
C:Accession: A28458; A27452; A23838; A39551; A28197; S06478; S02471  
R:Heuckeroth, R.O.; Birkenmeier, E.H.; Levin, M.S.; Gordon, J.I.  
J. Biol. Chem. 262, 9709-9717, 1987  
A:Title: Analysis of the tissue-specific expression, developmental regulation, and linkage of the rat fatty acid-binding protein gene  
A:Reference number: A28458; MUID: 87250640  
A:Accession: A28458  
A:Molecule type: mRNA  
A:Residues: 1-133 <HEU>  
A:Cross-references: GB:J02773; NID:g204077; PIDN:AAA41136.1; PID:g204078  
R:Claffey, K.P.; Herrera, V.L.; Brecher, P.; Ruiz-Opazo, N.  
Biochemistry 26, 7900-7904, 1987  
A:Title: Cloning and tissue distribution of rat heart fatty acid binding protein mRNA: 1-133  
A:Reference number: A27452; MUID:88107756  
A:Accession: A27452  
A:Molecule type: mRNA  
A:Residues: 1-133 <CLA>  
A:Cross-references: GB:M18034; NID:g204079; PIDN:AAA41137.1; PID:g204080  
Experimental source: heart  
R:Macchettini, J.C.; Said, B.; Schulz, H.; Gordon, J.I.  
J. Biol. Chem. 261, 8218-8223, 1986  
A:Title: Rat heart fatty acid-binding protein is highly homologous to the murine adipocyte fatty acid-binding protein  
A:Reference number: A23838; MUID:86250713  
A:Accession: A23838  
A:Molecule type: protein  
A:Residues: 'FEKN', 5-50, 'YG', 53-64, 'N', 65-70, 'D', 72-133 <SAC>  
A:Experimental source: heart  
R:Kimura, H.; Odani, S.; Nishi, S.; Sato, H.; Arakawa, M.; Ono, T.  
J. Biol. Chem. 266, 5963-5972, 1991  
A:Title: Primary structure and cellular distribution of two fatty acid-binding proteins  
A:Reference number: A39551; MUID:91170283  
A:Accession: A39551  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 10-69, 'Q', 71-121, 'D', 123-133 <KIN>  
A:Experimental source: kidney  
R:Gibson, B.W.; Yu, Z.; Aberth, W.; Burlingame, A.L.; Bass, N.M.  
J. Biol. Chem. 263, 4182-4185, 1988  
A:Title: Revision of the blocked N terminus of rat heart fatty acid-binding protein by 1-133  
A:Reference number: A28197; MUID:88153733  
A:Accession: A28197  
A:Molecule type: protein  
A:Residues: 2-10,46-53 <GIB>

R:Kanda, T.; Iseki, S.; Hitomi, M.; Kimura, H.; Odani, S.; Kondo, H.; Matsubara, Y.; Eur. J. Biochem. 185, 27-33, 1989  
A:Title: Purification and characterization of a fatty acid-binding protein from the g  
A:Reference number: S06478; MUID:90032682  
A:Accession: S06478  
A:Molecule type: protein  
A:Residues: 1-133 <KAN>  
A:Experimental source: stomach  
R:Jones, P.D.; Carne, A.; Bass, N.M.; Grigor, M.R.  
Biochem. J. 251, 919-925, 1988  
A:Title: Isolation and characterization of fatty acid binding proteins from mammary t  
A:Reference number: S02471; MUID:88326235  
A:Accession: S02471  
A:Molecule type: protein  
A:Residues: 16-22;32-45;54-59, 'XX', 62-63, 'X', 65-70;83-93;97-107;117-127 <JON>  
A:Experimental source: strain Wistar; mammary  
C:Superfamily: myelin p2 protein  
C:Keywords: acetylated amino end; cardiac muscle; heart; lipid binding; phosphoprotein  
F:1-133/Product: fatty acid-binding protein #status experimental <MAT>  
F:1/Modified site: acetylated amino end (Met) #status predicted

Query Match 70.7%; Score 477; DB 2; Length 133;  
Best Local Similarity 70.2%; Pred. No. 1.1e-36;  
Matches 92; Conservative 11; Mismatches 28; Indels 0; Gaps 0;  
QY 1 MCDAFVGTWKLVSSENFDDYKVGVPATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60  
DB 1 MADAFVGTWKLVSSENFDDYKSLGVPATRKQVASMTPPTTIKNGDITITIKHSTFKN 60  
QY 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKKRREDDKLWVECMV 120  
DB 61 TEISFQLGVEFDEVTADDRKVKSVVTLDDGKLHVQKWDGQETTLTRELSDGKLTLTLH 120  
QY 121 KGVVSTRVYER 131  
DB 121 GNVVSTRYK 131

RESULT 6  
PC4011  
fatty acid-binding protein - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 29-Jun-1995 #sequence\_revision 14-Jul-1995 #text\_change 13-Aug-1999  
C:Accession: PC4011; S04591; S05278; PC1248  
R:Treuner, M.; Kozak, C.A.; Gallahan, D.; Grosse, R.; Mueller, T.  
Gene 147, 237-242, 1994  
A:Title: Cloning and characterization of the mouse gene encoding mammary-derived grow  
A:Reference number: PC4011; MUID:95011621  
A:Accession: PC4011  
A:Molecule type: mRNA  
A:Residues: 1-133 <TRE>  
A:Cross-references: GB:U02884; NID:g409956; PIDN:AAA61933.1; PID:g409957  
R:Tweedie, S.; Edwards, Y.  
Nucleic Acids Res. 17, 4374, 1989  
A:Title: cDNA sequence for mouse heart fatty acid binding protein, H-FABP.  
A:Reference number: S04591; MUID:89296486  
A:Accession: S04591  
A:Molecule type: mRNA  
A:Residues: 1-33, 'G', 35-98, 'D', 100-133 <TWE>  
A:Cross-references: EMBL:X14961; NID:g51266; PIDN:CAA33084.1; PID:g51267  
R:Tweedie, S.; Edwards, Y.  
submitted to the EMBL Data Library, April 1989  
A:Reference number: S05278  
A:Accession: S05278  
A:Molecule type: mRNA  
A:Residues: 1-2, 'ER', 5-33, 'G', 35-98, 'D', 100-133 <TW2>  
A:Cross-references: EMBL:X14961  
A:Experimental source: cardiac  
R:Bansal, M.P.; Medina, D.  
Biochem. Biophys. Res. Commun. 191, 61-69, 1993  
A:Title: Expression of fatty acid-binding proteins in the developing mouse mammary gl

A:Reference number: PC1248; MUID:93191717

A:Accession: PC1248

A:Molecule type: protein

A:Residues: 23-108,'R',110-119 <BAN>

A:Experimental source: mammary gland

C:Comment: This protein functions as an endogenous growth inhibitor and differentiation

C:Genetics:

A:Gene: mdg1/h-fabp

A:Introns: 24/1; 82/2; 133/1

C:Superfamily: myelin P2 protein

C:Keywords: lipid binding

Query Match 69.0%; Score 466; DB 2; Length 133;

Best Local Similarity 67.9%; Pred. No. 1.2e-35;

Matches 89; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

Qy 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVIIKSESTFKN 60

Db 1 MADAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVIIKSESTFKN 60

Qy 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120

Db 61 TEINFOLGIEFDEVTADDRKVKSLVTLDDGGLIHVQKNGQETTLTRELVDGKLILTLH 120

Qy 121 KGVTSRTRYER 131

Db 121 GSVVSTRTRYEK 131

RESULT 7

MPH02

myelin P2 protein [validated] - human

N:Alternate names: peripheral myelin protein 2

C:Species: Homo sapiens (man)

C:Date: 05-Apr-1983 #sequence\_revision 27-Jan-1995 #text\_change 08-Dec-2000

A:Accession: J00977; A03143; S42424

R:Hayaaka, K.; Nanao, K.; Tahara, M.; Sato, W.; Takada, G.; Miura, M.; Uyemura, K.

Biochem. Biophys. Res. Commun. 181, 204-207, 1991

A:Title: Isolation and sequence determination of cDNA encoding P2 protein of human periph

A:Reference number: J00977; MUID:92068191

A:Accession: J00977

A:Molecule type: mRNA

A:Residues: 1-132 <HAY>

A:Cross-references: EMBL:X62167; NID:g35185; PIDN:CAA44096.1; PID:g35186

A:Experimental source: fetal spinal cord peripheral myelin

A:Note: authors did not translate the codon for residue 1

R:Suzuki, M.; Kitamura, K.; Sakamoto, Y.; Uyemura, K.

J. Neurochem. 39, 1759-1762, 1982

A:Title: The complete amino acid sequence of human P2 protein.

A:Reference number: A03143; MUID:83058785

A:Accession: A03143

A:Molecule type: protein

A:Residues: 2-98,'N',100-110,'D',112-132 <SUZ>

C:Comment: P2 protein and myelin basic protein together constitute a major fraction of P

C:Genetics:

A:Gene: GDB:PMP2

A:Cross-references: GDB:129030; OMIM:170715

A:Map position: 8q21.3-8q22.1

C:Superfamily: myelin P2 protein

C:Keywords: acetylated amino end; myelin; phosphoprotein

F:2-133/Product: myelin P2 protein #status experimental <MAT>

F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental

F:20/Binding site: phosphate (Tyr) (covalent) #status predicted

F:118-125/Disulfide bonds: #status experimental

Query Match 68.6%; Score 463; DB 1; Length 132;

Best Local Similarity 67.2%; Pred. No. 2.2e-35;

Matches 88; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

Qy 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVIIKSESTFKN 60

Db 1 MADAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVIIKSESTFKN 60

Db 1 MSNKFLGTWKLVSSENFDDYMKALGVGLATRKGLNLAKTPTVIISKGGDIITIRTESTFKN 60

Qy 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120

Db 61 TEISFKLGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120

Qy 121 KGVTSRTRYER 131

Db 121 KGVVCTRIYEK 131

RESULT 8

JH0407

myelin P2 protein - mouse

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 13-Aug-1999

A:Accession: JH0407

R:Narayanan, V.; Kaestner, K.H.; Tennekoon, G.I.

J. Neurochem. 57, 75-80, 1991

A:Title: Structure of the mouse myelin P2 protein gene.

A:Reference number: JH0407; MUID:91268811

A:Accession: JH0407

A:Molecule type: DNA

A:Residues: 1-132 <NAR>

A:Cross-references: GB:S39508; NID:g232319; PIDN:AAB19249.1; PID:g232320

C:Comment: This basic protein is found in peripheral and central nervous system myel

C:Genetics:

A:Introns: 25/1; 82/3; 116/3

C:Superfamily: myelin P2 protein

Query Match 66.7%; Score 450; DB 2; Length 132;

Best Local Similarity 64.9%; Pred. No. 3.4e-34;

Matches 85; Conservative 18; Mismatches 28; Indels 0; Gaps 0;

Qy 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVIIKSESTFKN 60

Db 1 MSNKFLGTWKLVSSENFDDYMKALGVGLANRKLGNLAKTPTVIISKGGDYITIRTESAFKN 60

Qy 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120

Db 61 TEISFKLGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120

Qy 121 KGVTSRTRYER 131

Db 121 KGVVCTRIYEK 131

RESULT 9

FZHUC

fatty acid-binding protein, cardiac and skeletal muscle - human

N:Alternate names: fatty acid-binding protein 3 (FABP3)

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1991 #sequence\_revision 03-May-1996 #text\_change 16-Jul-1999

C:Accession: S15432; JH0199; S00603; I54275; A27248

R:Peeters, R.A.; Veerkamp, J.H.; van Kessel, A.G.; Kanda, T.; Ono, T.

Biochem. J. 276, 203-207, 1991

A:Title: Cloning of the cDNA encoding human skeletal-muscle fatty-acid-binding protei

A:Reference number: S15432; MUID:91248148

A:Accession: S15432

A:Molecule type: mRNA; protein

A:Residues: 1-133 <PEE>

A:Cross-references: EMBL:X56549; NID:g31292; PIDN:CAA39889.1; PID:g31293

A:Experimental source: heart muscle; skeletal muscle

R:Boerchers, T.; Hojrup, P.; Nielsen, S.U.; Roepstorff, P.; Spener, F.; Knudsen, J.

Mol. Cell. Biochem. 98, 127-133, 1990

A:Title: Revision of the amino acid sequence of human heart fatty acid-binding protei

A:Reference number: JH0199; MUID:91094793

A:Accession: JH0199

A:Molecule type: protein

A:Residues: 2-129,'O',131-133 <BOE>

R:Offner, G.D.; Brecher, P.; Sawilovich, W.B.; Costello, C.E.; Troxler, R.F.

Biochem. J. 252, 191-198, 1988

[illegible]

Qy 121 KGVSTRVYER 131  
Db 121 GTAVCTRYEK 131

RESULT 12  
S06479  
fatty acid-binding protein, brain - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 24-Nov-1999  
C:Accession: S06479; JH0198  
R:Schoentgen, F.; Pignede, G.; Bonanno, L.M.; Jolles, P.  
Eur. J. Biochem. 185, 35-40, 1989  
A:Title: Fatty-acid-binding protein from bovine brain. Amino acid sequence and some properties  
A:Reference number: S06479; MUID:90032683  
A:Accession: S06479  
A:Molecule type: protein  
A:Residues: 1-131 <SCH>  
A:Experimental source: brain  
Note: 11-Val, 12-Asp, 14-Lys, 18-Asp, 33-Ala, 34-Ser, 40-Thr, 43-Glu, 44-Lys, 49-Val,  
R:Schoentgen, F.; Bonanno, L.M.; Pignede, G.; Jolles, P.  
Mol. Cell. Biochem. 98, 35-39, 1990  
A:Title: Amino acid sequence and some ligand binding properties of fatty acid-binding protein  
A:Reference number: JH0198; MUID:91094811  
A:Contents: annotation  
C:Comment: Synaptosomal Na+-dependent amino acid transport is stimulated by the fatty acid  
C:Superfamily: myelin P2 protein  
C:Keywords: blocked amino end  
F:1/Modified site: blocked amino end (Val) (probably acetylated) #status experimental

Query Match 63.0%; Score 425; DB 2; Length 131;  
Best Local Similarity 62.0%; Pred. No. 6.5e-32;  
Matches 80; Conservative 20; Mismatches 29; Indels 0; Gaps 0;

Qy 3 DAFVGTWKLVSSENFDDYMKVGVGFATPKVAGMAKPNMIISVNGDVITIKSESTFKNE 62  
Db 2 DAFVGTWKLVSSENFDDYMKVGVGFATPKVAGMAKPNMIISVNGDVITIKSESTFKNE 61

Qy 63 ISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVECEVM 122  
Db 62 ISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVECEVM 121

Qy 123 VTSTRVYER 131  
Db 122 VVAVRHYEK 130

RESULT 13  
A49184  
fatty acid-binding protein - chicken  
N:Alternate names: lipid-binding protein  
C:Species: Gallus gallus (chicken)  
C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 13-Aug-1999  
C:Accession: A49184; S26599  
R:Godbout, R.  
Exp. Eye Res. 56, 95-106, 1993  
A:Title: Identification and characterization of transcripts present at elevated levels in  
A:Reference number: A49184; MUID:93162137  
A:Accession: A49184  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-132 <GOD>  
A:Cross-references: EMBL:X65459; NID:g63230; PIDN:CAA46451.1; PID:g63231  
A:Experimental source: retina  
A:Note: sequence extracted from NCBI backbone (NCBIP:124757)  
C:Superfamily: myelin P2 protein

Query Match 58.1%; Score 392; DB 2; Length 132;  
Best Local Similarity 56.1%; Pred. No. 6.9e-29;  
Matches 74; Conservative 19; Mismatches 39; Indels 0; Gaps 0;

Qy 1 MCDAFVGTTWKLVSSENFDDYMKVGVGFATPKVAGMAKPNMIISVNGDVITIKSESTFKN 60  
Db 1 MVEAFCATWKLADSHNFDEYMKALGVGFAMRQGVNVTPTVTIISSEGDKVVIRTQSTFKN 60

Qy 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVECEVM 120  
Db 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVECEVM 120

Qy 121 KGVSTRVYER 132  
Db 121 GDVAVRHYERA 132

RESULT 14  
I52524  
testis lipid binding protein - rat  
N:Alternate names: 15 kDa perforatorial protein PERF 15  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 13-Aug-1999  
C:Accession: I52524; I53089  
R:Schmitt, M.C.; Jamison, R.S.; Orgebin-Crist, M.C.; Ong, D.E.  
Biol. Reprod. 51, 239-245, 1994  
A:Title: A novel, testis-specific member of the cellular lipophilic transport protein  
A:Reference number: I52524; MUID:95035569  
A:Accession: I52524  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-132 <RES>  
A:Cross-references: EMBL:U07870; NID:g469051; PIDN:AAA68627.1; PID:g469052  
R:Oko, R.J.; Morales, C.C.; Oko, R.; Morales, C.R.  
Dev. Biol. 166, 235-245, 1994  
A:Title: A novel testicular protein, with sequence similarities to a family of lipid  
A:Reference number: I53089; MUID:95046905  
A:Accession: I53089  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-132 <RE2>  
A:Cross-references: EMBL:U09022; NID:g538268; PIDN:AAA67873.1; PID:g538269  
C:Superfamily: myelin P2 protein

Query Match 57.8%; Score 390; DB 2; Length 132;  
Best Local Similarity 56.5%; Pred. No. 1.1e-28;  
Matches 74; Conservative 26; Mismatches 31; Indels 0; Gaps 0;

Qy 1 MCDAFVGTTWKLVSSENFDDYMKVGVGFATPKVAGMAKPNMIISVNGDVITIKSESTFKN 60  
Db 1 MIEPFLGTWKLVSSENFENYRELGVCEPRKACLIKPSVISFNGERMDIQAGSACRN 60

Qy 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVECEVM 120  
Db 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVECEVM 120

Qy 121 KGVSTRVYER 131  
Db 121 NNWVSTRTYER 131

RESULT 15  
I56510  
fatty acid binding protein - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 13-Aug-1999  
C:Accession: I56510  
R:Bennett, E.; Stenvers, K.L.; Lund, P.K.; Popko, B.  
J. Neurochem. 63, 1616-1624, 1994  
A:Title: Cloning and characterization of a cDNA encoding a novel fatty acid binding p  
A:Reference number: I56510; MUID:95016702  
A:Accession: I56510  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-132 <RES>

A:Cross-references: EMBL:U02096; NID:g476081; PIDN:AAA60455.1; PID:g476082  
C:Superfamily: myelin P2 protein

Query Match	57.0%	Score 385;	DB 2;	Length 132;
Best Local Similarity	55.3%	Pred. No. 3e-28;		
Matches 73;	Conservative 19;	Mismatches 40;	Indels 0;	Gaps 0;

  

QY	1	MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN	60
Db	1	MVDAFCATWKLTDQNFDEYMKALGVGFATRKQVGNVTKPTVIIISQEGGKVVIRTQCTFKN	60
QY	61	TEISFILGQEFDEVTDADDRVKSTITLDGGVLVHVQKWDGKSTTIKKREDDKLVVECV	120
Db	61	TEISFQLGEEFEETSIDDRNCKSVIRLDGKLIHVQKWDGKSTTIKKREDDKLVVECV	120
QY	121	KGVTSTRVYERA	132
Db	121	GDVVAVRCYEKA	132

Search completed: June 7, 2002, 18:20:10  
Job time: 152 sec





Db		1	MADAFVCTWKLVDKSNFDDYMKSLGVGFATQVASMFKPTTIIIEKNGDITTIKTQTSTFN	60
Qy	61	TEISFILQBFEDVTDADRKKVTIILDGGVLVHVOKWGDKSTTKRKREDDKLVCEVM	120	
Db	61	TEINFQLGIFEDVTDADRKKVSLTVLDGGKLHVOKWNGQETLTRELVDGKLILTLTH	120	
Qy	121	KGVTSRTRYER	131	
Db	121	GSVVSTRTYEK	131	

```

RESULT 2
US-08-470-298B-7
; Sequence 7, Application US/08470298B
; Patent No. 5844081
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: YU, GUO-LIANG
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: CYTOSTATIN I
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850

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	Query Match	69.0%;	Score 466;	DB 2;	Length 131;
	Best Local Similarity	67.9%;	Pred. No. 6.3e-49;	Mismatches 89;	Conservative 15;
					Gaps 0;
QY	1	MCDAFVGTWKLVSSENFDDYMKKEVGCGFATRKVAGNAKPMILISVNGDVITIKSSTFKN	60	:           :           :           :           :	
Dd	1	MADAFCVTGWTGLVDKNPFDDYMKSGLGVGFATRQVASMTKETTTIENKGDITTIKTOSTFKN	60	:           :           :           :           :	
QY	61	TEISFILGQBFEDEVTADRRKRKVSTITLDGGVLHVHGWDGSKSTTKRKRREDDKLVCEVM	120	:           :           :           :           :	
Dd	61	TEINFOLGIEFDEVTAADDRKKVKSLVTDGGKLIHQKWKGQETTLTRELVDGKLILTLT	120	:           :           :           :           :	
QY	121	KGYTSRTVRYY	131	:	
Dd	121	GSVVSTRTYEK	131	:	

```

RESULT 3
US-08-820-825-11
; Sequence 11, Application US/08820825
; Patent No. 5945309
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/820.825
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-820-825-11

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Query Match          69.0% ; Score 466; DB 2; Length 133;
Best Local Similarity 67.9% ; Pred. No. 6.4e-49;
Matches 89; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

Qy 1 MDAFVGTWKLVSSENDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MADAFVGTWKLVDKSNFDDYMKSLGVGFATRQVASMKTPTTILEKNGDTITIKQSTFKN 60

Qy 61 TEISFILGOEDEVTAADRKKVKSITITLDGGVLVHVQKWDGCKSTTIKRRDDDKLWVECV 120
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 TEINFQIGIEFDEVTAADRKKVKS LVTLDGGKLIIHVQKWNGOETTTLRELVDGKLILTL 120

Qy 121 KGVSTRVYER 131
   | | | | | | | |
Db 121 GSVVSTRYEK 131

RESULT 4
US-09-023-073A-7
; Sequence 7, Application US/09023073A
; Patent No. 5977309
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Rosen, Craig A
; TITLE OF INVENTION: Cytostatin I
; NUMBER OF SEQUENCES: 11

```



```

CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MARYLAND
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,073A
FILING DATE: 13-FEB-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Wales, Michele M.
REGISTRATION NUMBER: P-43,975
REFERENCE/DOCKET NUMBER: PFI75D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5772
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-023-073A-7

Query Match 69.0%; Score 466; DB 2;
Best Local Similarity 67.9%; Pred. No. 6,4e-49;
Matches 89; Conservative 15; Mismatches 27;

QY 1 MDAFVGTWKLVSSENFDDYMKVEGVGFATRKVAGMAKPNMIIS
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MADAFVGTWKLVDKSNFDDYMKSLGVSFGFATRVASMTKPTTIEE
| | | | | | | | | | | | | | | | | | | | | | | | | |

QY 61 TELTSFILGQEFDEVTDADRKKVASTITLDGGVLVHVQKWDGKSTT
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 TEINFQLGIEFDEVTDADRKKVSLVTLTDGGLKLIHVQKWNGQETT
| | | | | | | | | | | | | | | | | | | | | | | | | |

QY 121 KGVTSRTRYER 131
| | | | |
Db 121 GSVSTRYEK 131
| | | | |

RESULT 5
US-09-307-817-11
Sequence 11, Application US/09307817
Patent No. 6232291
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER L.
APPLICANT: DILLON, PATRICK
TITLE OF INVENTION: CYTOSTATIN III
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/307,817
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/820,825
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PE222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-307-817-11

Query Match 69.0%; Score 4
Best Local Similarity 67.9%; Pred. N
Matches 89; Conservative 15; Mism:

QY 1 MCDAPVGTWKLVSSENFDDYMKVEGVGVGFATRR
| | | | | | | | | | | | | | | | | | | | |
Db 1 MADAPVGTWKLVDKSNFDDYMKSLGSLGVGFATRR
| | | | | | | | | | | | | | | | | | | | |
QY 61 TEISFILGQEFDEVTAADDRKVKSTFTLDGCV
| | | | | | | | | | | | | | | | | | | | |
Db 61 TEINFQLGIEFDEVTAADDRKVKSLVTLDGSK
| | | | | | | | | | | | | | | | | | | | |
QY 121 KGVSTRVYR 131
| | | | |
Db 121 GSVVSTRVYK 131

RESULT 6
US-09-361-737-7
; Sequence 7, Application US/09361737
; Patent No. 6287812
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Rosen, Craig A
; TITLE OF INVENTION: Cytostatin I
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES,
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/361,737
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/023,073
; FILING DATE: 13-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Wales, Michele M.

```

REGISTRATION NUMBER: P-43,975  
REFERENCE/DOCKET NUMBER: PF175D2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-610-5772  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-361-737-7

Query Match 69.0%; Score 466; DB 4; Length 133;  
Best Local Similarity 67.9%; Pred. No. 6.4e-49;  
Matches 89; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 MCDAFVGTWKLVSSENFDDYMKYGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60  
DB 1 MADAFVGTWKLVSSENFDDYMKYGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60  
QY 61 TEISFILGOEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRRDDKLVEECVM 120  
DB 61 TEINFLQIEFDEVTADDRKVKSLVTLDDGGLIHVQKWDGKSTTIKRRDDKLVEECVM 120

QY 121 KGVSTRTVRYER 131  
DB 121 GSVVSTRTYER 131

RESULT 7  
US-08-409-731A-11  
Sequence 11, Application US/08409731A  
Patent No. 5658758  
GENERAL INFORMATION:  
APPLICANT: Ni, Jian  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Gentz, Reiner  
APPLICANT: Rosen, Craig A.  
TITLE OF INVENTION: CYTOSTATIN I  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: USA  
ZIP: 20850

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/409,731A  
FILING DATE: 24-MAR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Benson, Robert H  
REGISTRATION NUMBER: 30,446  
REFERENCE/DOCKET NUMBER: PF175  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8512  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 132 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-409-731A-11

Query Match 68.6%; Score 463; DB 1; Length 132;  
Best Local Similarity 67.2%; Pred. No. 1.5e-48;  
Matches 88; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

QY 1 MCDAFVGTWKLVSSENFDDYMKYGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60  
DB 1 MSNKFLGTWKLVSSENFDDYMKALGVGLATRKLGKLNLAQPTVIISKGGDIITIRTESTFKN 60  
QY 61 TEISFILGOEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRRDDKLVEECVM 120  
DB 61 TEISFKLGOEFDEVTADNRKTSIVTLQSGSLNVQVQWMDGKETTIIKRLVNGKVMVAECKM 120

QY 121 KGVSTRTVRYER 131  
DB 121 KGVVCTRIYER 131

RESULT 8  
US-08-470-298B-11  
Sequence 11, Application US/08470298B  
Patent No. 5844081  
GENERAL INFORMATION:  
APPLICANT: NI, JIAN  
APPLICANT: GENTZ, REINER  
APPLICANT: YU, GUO-LIANG  
APPLICANT: ROSEN, CRAIG A.  
TITLE OF INVENTION: CYTOSTATIN I  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/470,298B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BROOKES, ALLAN A.  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF175D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8512  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 132 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: MYELIN P2 (FIGURE 2)  
US-08-470-298B-11

Query Match 68.6%; Score 463; DB 2; Length 132;  
Best Local Similarity 67.2%; Pred. No. 1.5e-48;  
Matches 88; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

QY 1 MCDAFVGTWKLVSSENFDDYMKYGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60  
DB 1 MSNKFLGTWKLVSSENFDDYMKALGVGLATRKLGKLNLAQPTVIISKGGDIITIRTESTFKN 60





```

Best Local Similarity   64.98;  Pred. No. 7.4e-47;
Matches 85;  Conservative 16;  Mismatches 30;  Indels 0;  Gaps 0;

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      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1  MVDAFLGTWKLVDKSNDDYMKSLGVGFATRQVASMKPTTIEKNGDILTLKTHSTFKN 60

QY      61  TETSFILGQGFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRKREDDKLWVEVCVM 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61  TETSFILGVGFDEVTADDRKVKSVITLDGGKLVHLQKWGQETTLVRELIDGKILTLTH 120

QY      121  KGVTSSTRVYER 131
      |||:||||:
Db      121  GTAVCTRTYEK 131

RESULT 15
US-09-307-817-13
; Sequence 13, Application US/09307817
; Patent No. 6232291
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: YU, GUO-LIANG
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III

```

```

CORRESPONDENCE ADDRESS:
ADDRESS: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/307,817
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/820,825
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF222
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-307-817-13

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QY 6I TEISFILGQEDEVITADDRKVKSTITLDGGVLVHVQRWDGKSTTKRRREDDKLVECV 120  
||||| ||||| ||||| :||||| ||||| :||| : ||| ::  
||||| ||||| ||||| :||||| ||||| :||| : ||| ::

Db 61 TEISFKLGVEFDETTADDRKVKSIVTLDGGKLVHLQKWGOETTIVRELIDGKLILTLTH 120  
Qy 121 KGVSTSTRVYER 131  
|| ||:  
Db 121 GTAVCTRTYEK 131

Search completed: June 7, 2002, 18:19:47  
Job time: 164 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2002, 18:13:28 ; Search time 30.07 Seconds  
(without alignments)  
487.587 Million cell updates/sec

Title: US-09-503-596-4

Perfect score: 675

Sequence: 1 MCDAFVGTWKLVSSENFDDY.....KLVECMKGVSTRVIERA 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	675	100.0	132	21	AA190320 Human AFABP protei
2	625	92.6	132	21	AA190319 Mouse AFABP protei
3	466	69.0	133	22	AAG66576 Mouse MDGI polyep
4	458	67.9	136	19	AAW40227 Human myelin P2 pr
5	453	67.1	131	12	AA133559 MDGI active peptid
6	449	66.5	133	22	AAG66578 Human MDGI polyep
7	446	66.1	133	22	AAG66577 Bovine MDGI polyep
8	445	65.9	136	19	AAW40228 Bovine myelin P2 p
9	435.5	64.5	134	18	AAW31534 Porcine heart-fatt
10	399	59.1	132	18	AAW22408 Human cytoctatin I
11	399	59.1	132	19	AAW80949 Amino acid sequenc

12	399	59.1	132	19	AAW81106 Human cytoctatin I
13	399	59.1	132	20	AAW82403 Human 14-16 kDa FA
14	396	58.7	117	21	AAAG03847 Human secreted pro
15	386.5	57.3	131	22	AAG66580 Human cytoctatin I
16	382	56.6	132	21	AAAG03957 Human secreted pro
17	381	56.4	132	16	AAW75423 Mouse cellular X b
18	375	55.6	88	21	AAW58740 Breast and ovarian
19	366	54.2	135	15	AAW58666 Melanogenic inhibi
20	366	54.2	135	22	AAU08674 Human keratinocyte
21	362	53.6	135	22	AAU08673 Mouse keratinocyte
22	361	53.5	158	22	ABG27577 Novel human diagno
23	360	53.3	82	22	AAW75123 Human colon cancer
24	298.5	44.2	134	22	AAU08666 Human NOV10 protei
25	298.5	44.2	163	22	AAU08665 Cytoctatin family
26	297	44.0	132	22	AAU10066 Cytoctatin family
27	297	44.0	130	22	ABW62690 Drosophila melanog
28	285	42.2	130	22	ABW62690 Human 5' EST relat
29	270	40.0	69	21	AAW65303 Human retinoid bin
30	237	35.1	134	20	AAW68550 Fatty acid-binding
31	232.5	34.4	172	22	AAU10059 Schistosoma manso
32	229.5	34.0	133	16	AAW75643 CRABP-I gene produ
33	222	32.9	137	14	AAW42212 Human secreted pro
34	210	31.1	56	21	AAW01405 CRABP-II gene prod
35	201.5	29.9	138	14	AAW42211 Human lung tumour
36	201.5	29.9	138	22	AAW76852 Lung cancer associ
37	201.5	29.9	149	21	AAW58158 Human secreted pro
38	194	28.7	99	21	AAW01603 Novel human diagno
39	191.5	28.4	181	22	ABG13617 Human cancer assoc
40	186	27.6	160	21	AAW43403 Novel human diagno
41	169.5	25.1	176	22	ABG26878 Human polypeptide
42	165	24.4	135	22	AAW38758 Human cellular ret
43	165	24.4	135	22	AAW60659 Human polypeptide
44	165	24.4	168	22	AAW40544 Human cytoctatin I
45	164	24.3	135	18	AAW30891

ALIGNMENTS

RESULT	1
AA190320	
ID	AA190320 standard; Protein; 132 AA.
XX	
AC	AA190320;
XX	
DT	22-NOV-2000 (first entry)
XX	
DE	Human AFABP protein sequence.
XX	
KW	AFABP; adipocyte fatty acid binding protein; atherosclerotic lesion;
KW	lesion formation inhibition; macrophage; adipocyte; atherosclerosis;
KW	serum cholesterol; therapy; human.
XX	
OS	Homo sapiens.
XX	
PN	WO2000047734-A1.
XX	
PD	17-AUG-2000.
XX	
PF	11-FEB-2000; 2000WO-US03560.
XX	
PR	12-FEB-1999; 99US-0119880.
XX	
PA	(HARD ) HARVARD COLLEGE.
XX	
PI	Lee M, Perrella MA, Hotamisligil GS;
XX	
DR	WPI: 2000-506094/45.
DR	N-PSDB; AAA37717.
XX	
PT	Reducing expression of adipocyte fatty acid binding protein through
PT	administration of a compound is used to inhibit formation of an
PT	atherosclerotic lesion -

XX Disclosure; Page 14; 43pp; English.  
 XX This sequence represents the human AFABP (adipocyte fatty  
 CC acid binding protein) protein sequence. The invention relates to a method  
 CC for inhibiting formation of an atherosclerotic lesion comprising  
 CC administering to a mammal a compound that reduces expression of adipocyte  
 CC fatty acid binding protein (AFABP). The method is used to inhibit  
 CC formation of atherosclerotic lesions. The method is used to inhibit  
 CC compounds which can be used to inhibit formation of atherosclerotic  
 CC lesions through inhibition of AFABP binding to an intracellular ligand  
 CC in a macrophage or adipocyte, inhibition of development of an  
 CC atherosclerotic lesion, inhibition of a macrophage differentiating into  
 CC a foam cell or inhibition of AFABP expression in a cell. AFABP activity  
 CC may be inhibited to treat atherosclerosis or to treat individuals at risk  
 CC of developing atherosclerosis. Inhibiting AFABP expression or activity  
 CC reduces the development of atherosclerotic lesions despite a high level  
 CC of serum cholesterol.  
 XX  
 XX Sequence 132 AA;  
 SQ

Query Match 100.0%; Score 675; DB 21; Length 132;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-71;  
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCDAPVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60  
 Db 1 mcdafvgtwklvsseanfddymkevvgvfatrkvagmakpnmiisvngdvitikestfkn 60

Qy 61 TEISFILGOEFDEVTTADDRKVKSTITLDGVLVHVQKWDGKSTTIKKREDDKLVVECV 120  
 Db 61 teisfilgqefdevttadrrkstkstltldggvlvvhvqkwdgksttikrreddklvvecv 120

Qy 121 KGVTSRVYERA 132  
 Db 121 kgvtstrvyera 132

RESULT 2  
 AAY90319  
 ID AAY90319 standard; Protein; 132 AA.  
 XX  
 AC AAY90319;  
 XX  
 DT 22-NOV-2000 (first entry)  
 XX  
 DE Mouse AFABP protein sequence.  
 XX  
 KW AFABP; adipocyte fatty acid binding protein; atherosclerotic lesion;  
 KW lesion formation inhibition; macrophage; adipocyte; atherosclerosis;  
 KW serum cholesterol; therapy; mouse.  
 XX  
 OS Mus sp.  
 XX  
 PN WO200047734-A1.  
 XX  
 PD 17-AUG-2000.  
 XX  
 PF 11-FEB-2000; 2000WO-US03560.  
 XX  
 PR 12-FEB-1999; 99US-0119880.  
 XX  
 PA (HARD ) HARVARD COLLEGE.  
 XX  
 PI Lee M, Ferrella MA, Hotamisligil GS;  
 XX  
 DR WPI; 2000-506094/45.  
 DR N-PSDB; AAA37716.  
 XX  
 XX Reducing expression of adipocyte fatty acid binding protein through  
 PT administration of a compound is used to inhibit formation of an  
 PT atherosclerotic lesion -

XX Disclosure; Page 14; 43pp; English.  
 XX This sequence represents the mouse AFABP (adipocyte fatty  
 CC acid binding protein) protein sequence. The invention relates to a method  
 CC for inhibiting formation of an atherosclerotic lesion comprising  
 CC administering to a mammal a compound that reduces expression of adipocyte  
 CC fatty acid binding protein (AFABP). The method is used to inhibit  
 CC formation of atherosclerotic lesions. The method is used to identify  
 CC compounds which can be used to inhibit formation of atherosclerotic  
 CC lesions through inhibition of AFABP binding to an intracellular ligand  
 CC in a macrophage or adipocyte, inhibition of development of an  
 CC atherosclerotic lesion, inhibition of a macrophage differentiating into  
 CC a foam cell or inhibition of AFABP expression in a cell. AFABP activity  
 CC may be inhibited to treat atherosclerosis or to treat individuals at risk  
 CC of developing atherosclerosis. Inhibiting AFABP expression or activity  
 CC reduces the development of atherosclerotic lesions despite a high level  
 CC of serum cholesterol.  
 XX  
 XX Sequence 132 AA;  
 SQ

Query Match 92.6%; Score 625; DB 21; Length 132;  
 Best Local Similarity 91.7%; Pred. No. 4.1e-65;  
 Matches 121; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MCDAPVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60  
 Db 1 mcdafvgtwklvsseanfddymkevvgvfatrkvagmakpnmiisvngdvitirsetfkn 60

Qy 61 TEISFILGOEFDEVTTADDRKVKSTITLDGVLVHVQKWDGKSTTIKKREDDKLVVECV 120  
 Db 61 teisfilgqefdevttadrrkstkstltldggvlvvhvqkwdgksttikrreddklvvecv 120

Qy 121 KGVTSRVYERA 132  
 Db 121 kgvtstrvyera 132

RESULT 3  
 AAG66576  
 ID AAG66576 standard; Protein; 133 AA.  
 XX  
 AC AAG66576;  
 XX  
 DT 22-OCT-2001 (first entry)  
 XX  
 DE Mouse MDGI polypeptide.  
 XX  
 KW Mouse; cytoostatin III; cytoostatic; epithelial cell growth;  
 KW milk production; breast involution; cardiac myocyte hypertrophy;  
 KW leukaemia; MDGI; mammary-derived growth inhibitor.  
 XX  
 OS Mus sp.  
 XX  
 PN USG232291-B1.  
 XX  
 PD 15-MAY-2001.  
 XX  
 PF 10-MAY-1999; 99US-0307817.  
 XX  
 PR 19-MAR-1996; 96US-0013655.  
 PR 19-MAR-1997; 97US-0820825.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI NI J, Yu G, Gentz R, Dillon PJ;  
 XX  
 DR WPI; 2001-342775/36.  
 XX  
 XX Cytostatin III polypeptides that modulate growth of epithelial cells,  
 PT stimulate milk production in humans and cows and promote involution of  
 PT breast, for research, biological, clinical and therapeutic purposes -









Sequence 132 AA;

Query Match 59.1%; Score 399; DB 18; Length 132;  
Best Local Similarity 56.8%; Pred. No. 1.1e-38;

Qy	1	MCDAFVCTWKLIVSENFDDYMKVGVGFATRKVAGNAKNMIIISVNGVDVITIKSESTFKN	60
Db	1	msaefcatwkltsnfnfdeymkaigvgfacygnvckpcvllisqegdkvrltstcfkn	60
Qy	61	TEISFILGQEFDEVTAADRRVKVSTIYLDGVLVHVQKQDGCKSTYIKRRBKDKLVVECVYM	120
Db	61	teisfilgsefdettadrrcnsvslldgdklvhlqgdgketcfnvrekldgkmvmtltf	120
Qy	121	KGVTSTRVYERA	132
Db	121	gdvvavrhyeka	132

RESULT 11

AAW80949  
ID AAW80949 standard; Protein; 132 AA.

AAW80949:

DT 16-FEB-1999 (first entry)

DE Amino acid sequence of the human fatty acid binding protein.

Human; fatty acid binding protein; Hu-FABP; developmental disorder;  
cancer; spina bifida; hydrocephalus; hereditary neuropathy;  
Charcot-Marie-Tooth disease; neurofibromatosis; antagonist;  
hyperalgesia; adenocarcinoma.

OS Homo sapiens.

XX  
PN  
W09845440-A1

XX  
PD  
15-000-1998XX  
DE 09-APR-1000.

XX  
00-800-1007-  
0770-605703

XX  
XX

XX

XX

DR N-PSDB; AAV68587.

PT New isolated human f

PT disorders, epilepsy

Claim 1: Fig 1: 59pp

xx This is the amino acid sequence

protein (Hu-FABP) used in the method of the invention, the Hu-FABP, plays a role in developmental disorders and cellular development and differentiation, including cancers. The Hu-FABP can be used for treating developmental disorders, e.g. spina bifida, hydrocephalus, and hereditary neuropathies such as Charcot-Marie-Tooth disease and neurofibromatosis. Antagonists to the Hu-FABP can be used for treating a disorder associated with cellular development and differentiation, e.g. hyperaldosteronism, and cancers including

**RESULT 10**

ID AAW22408 standard; Protein; 132 AA.

AC AAW22408;

DT 02-OCT-19

Human cytostatin II.

Cytostatin II: tumour: cancer: angiogenesis: lactation:

KW  
XX  
therapy.

US Homo sapiens.  
YY

WO9711970-A1.

PD 03-APR-1997.

PF 29-SEP-1995; 95WO-US12540.

PR 29-SEP-1995; 95WO-US12540.

PA (HUMA-) HUMAN GENOME SCI INC

PI Gentz R, Ni J, Yu G;

DR WPI; 1997-212854/19.

XX  
XX  
TJ/TW/0001 N

PT human cyclosporin cellular growth a

XX  
FI and angrogenesisPS Disclosure; Fig 1; /1pp; English.  
xx

human cytotactin II (AAW22408) is related by amino sequence homology to mammary derived growth inhibitor found in cattle and mice. Its amino acid sequence was deduced from a cDNA clone (AR74751) obtd. from a foetal brain library. Recombinant cytotactin II can be expressed in prokaryotic or eukaryotic host cells. It can be used





Job time: 360 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 8, 2002, 09:32:01 ; Search time 2892.64 Seconds  
(without alignments)  
2416.970 Million cell updates/sec

Title: US-09-503-596-8  
Perfect score: 518  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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  - 2: em\_esthum:\*
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  - 6: em\_estpl:\*
  - 7: em\_estro:\*
  - 8: em\_hic:\*
  - 9: gb\_estl:\*
  - 10: gb\_est2:\*
  - 11: gb\_hic:\*
  - 12: gb\_gss:\*
  - 13: em\_gss\_hum:\*
  - 14: em\_gss\_inv:\*
  - 15: em\_gss\_pln:\*
  - 16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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3	52.8	10.2	1044	12	AG056564
4	47.6	9.2	987	12	CNS00418
5	47	9.1	774	12	CNS01FGX
6	45.6	8.8	1101	12	CNS017RP
7	45.6	8.8	1123	10	BE036673
8	45.4	8.8	1031	9	BE036673
9	44.6	8.6	1246	12	AG135261
10	44.4	8.6	667	12	AZ370954
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12	44.2	8.5	875	10	BF264737
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14	43.8	8.5	621	10	BI390101
15	43.8	8.5	1322	10	BE966081
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17	43.4	8.4	322	12	CNS00HDD

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C 19	43.4	8.4	877	12	CNS00D37
C 20	43.4	8.4	1101	12	CNS002BV
C 21	43.2	8.3	1080	12	AG130798
C 22	43	8.3	539	9	AV685047
C 23	43	8.3	561	12	AZ886506
C 24	42.8	8.3	389	12	CNS03YLI
C 25	42.8	8.3	477	12	AQ390696
C 26	42.8	8.3	586	12	AQ390699
C 27	42.8	8.3	1152	12	AQ779752
C 28	42.6	8.2	590	12	BH012597
C 29	42.6	8.2	787	10	BG113790
C 30	42.4	8.2	407	12	AZ083954
C 31	42.4	8.2	580	10	BE274509
C 32	42.4	8.2	715	10	BG495803
C 33	42.4	8.2	1000	12	AG042808
C 34	42.2	8.1	497	9	AI222742
C 35	42.2	8.1	565	10	BM439556
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C 37	42.2	8.1	611	9	AL588140
C 38	42	8.1	543	12	AQ500504
C 39	42	8.1	597	9	AV762619
C 40	42	8.1	743	12	B20664
C 41	42	8.1	971	12	CNS006JC
C 42	42	8.1	1101	12	CNS007MD
C 43	41.8	8.1	520	12	AZ365733
C 44	41.8	8.1	1101	12	CNS00F86
C 45	41.6	8.0	923	12	AZ205171

## ALIGNMENTS

RESULT 1

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

CNS005TE 997 bp DNA linear GSS 03-JUN-1999  
Drosophila melanogaster genome survey sequence TET3 end of BAC #  
BAC12K22 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

AL060767

AL060767.1 GI:4943573

GSS

fruit fly.

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 997)

Genoscope.

Direct Submission

Submitted (02-JUN-1999)

Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see <http://www.fruitfly.org> The BDGP Drosophila

Melanogaster BAC library was prepared by Kazutoyo Osogawa and

Aaron Mamoser in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial

ECORI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain y2; cn bw sp, the same strain used for the BDGP's

p1 and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be

found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

Location/Qualifiers

1. .997

/organism="Drosophila melanogaster"

/db\_xref="taxon:7227"

/clone\_lib="RPCI-98"

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/clone_lib="RPCI-98"
/clone="BACR30X03"
/note="end : TE13"

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/clone="PTB-042005.R"
/sex="male"
/cell_type="lymphoblast"

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	/clone_tlb="PTB Chimpanzee Male BAC Library"					
BASE COUNT	573 a	91 c	293 g	27 t	60 others	















GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 8, 2002, 09:33:56 ; Search time 102.09 Seconds  
(without alignments)  
1246.333 Million cell updates/sec

Title: US-09-503-596-8  
Perfect score: 518  
Sequence: 1 gaattccagcaggaatcagg.....ccctgggtcttctcttaga 518

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents.NA.\*  
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2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	74.2	14.3	7218	1	US-08-232-463-14
4	41	7.9	41	1	US-07-771-022F-16
5	40.6	7.8	72604	4	US-09-268-992-7
6	39.6	7.6	6042	1	US-08-261-822A-1
7	39.6	7.6	6042	5	PCT-US95-07744A-1
8	39.6	7.6	6172	4	US-08-819-288-1
9	39.6	7.6	6172	4	US-09-400-348-1
10	38.8	7.5	289	4	US-09-007-003-17
11	38.8	7.5	289	4	US-09-244-796-17
12	38.2	7.4	372	4	US-09-018-584A-13
13	38.2	7.4	152331	3	US-09-128-155-16
14	38.2	7.4	176373	3	US-09-128-155-17
15	36.6	7.1	5433	3	US-08-929-329-1
16	36.4	7.0	2389	3	US-08-691-563C-52
17	36	6.9	333	4	US-09-018-584A-27
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19	35.6	6.9	29604	3	US-08-781-891-207
20	35.4	6.8	597	2	US-08-332-766A-19
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25	34.6	6.7	291	1	US-08-074-275-7
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C 30	34.2	6.6	243	1	US-07-799-828C-9	Sequence 9, Appl
C 31	34.2	6.6	243	1	US-08-074-275-9	Sequence 9, Appl
C 32	34.2	6.6	243	1	US-08-480-366-9	Sequence 9, Appl
C 33	34.2	6.6	243	2	US-07-952-277A-9	Sequence 9, Appl
C 34	33.4	6.4	3892	2	US-08-555-723B-3	Sequence 3, Appl
C 35	33.4	6.4	3892	3	US-09-123-465-3	Sequence 3, Appl
C 36	33	6.4	33	1	US-07-771-022F-15	Sequence 15, Appl
C 37	32.8	6.3	1859	3	US-08-691-563C-46	Sequence 46, Appl
C 38	32.4	6.3	569	2	US-08-485-778-5	Sequence 5, Appl
C 39	32.4	6.3	2791	4	US-09-570-367C-1	Sequence 1, Appl
C 40	32.4	6.3	80246	4	US-09-078-294-4	Sequence 4, Appl
C 41	32.4	6.3	80595	4	US-09-078-294-3	Sequence 3, Appl
C 42	32.2	6.2	394	2	US-08-623-908A-7	Sequence 7, Appl
C 43	32.2	6.2	533	6	5482709-5	Patent No. 5482709
C 44	32.2	6.2	152331	3	US-09-128-155-16	Sequence 16, Appl
C 45	32	6.2	1559	4	US-09-019-095A-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1  
US-07-771-022F-1  
; Sequence 1, Application US/07771022F  
; Patent No. 5476926  
; GENERAL INFORMATION:  
; APPLICANT: SPIEGELMAN, BRUCE M.  
; APPLICANT: GRAVES, REED A.  
; APPLICANT: ROSS, SUSAN R.  
; TITLE OF INVENTION: Adipocyte-Specific DNA  
; TITLE OF INVENTION: Sequences And Use Thereof In The Production Of  
; TITLE OF INVENTION: Transgenic Animals Exhibiting Altered Fat  
; TITLE OF INVENTION: Tissue Metabolism.  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Dana-Farber Cancer Institute  
; STREET: 44 Binney Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02115

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1 MB storage  
COMPUTER: IBM-compatible Compaq Prolinea MT 4/66  
OPERATING SYSTEM: MS/DOS  
SOFTWARE: WordPerfect 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07771,022F  
FILING DATE: 07-OCT-1991  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/589,971  
FILING DATE: 28-SEP-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: HART, JULIA D.  
REGISTRATION NUMBER: 33132  
REFERENCE/DOCKET NUMBER: DFCI-117  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 632-4016  
TELEFAX: (617) 632-4012  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 518 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
HYPOTHETICAL: no  
ANTI-SENSE: no  
ORIGINAL SOURCE:  
ORGANISM: Mus musculus



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Qy 323 gacgactctatgctccctctttctgtgattttcatgttctgagctcttttcccccg 382
Db 1224 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY
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RESULT 4
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; Sequence 16, Application US/07771022F
; Patent No. 5476926
; GENERAL INFORMATION:
; APPLICANT: SPIEGELMAN, BRUCE M.
; APPLICANT: GRAVES, REED A.
; APPLICANT: ROSS, SUSAN R.
; TITLE OF INVENTION: Adipocyte-Specific DNA
; TITLE OF INVENTION: Sequences And Use Thereof In The Production Of
; TITLE OF INVENTION: Transgenic Animals Exhibiting Altered Fat
; TITLE OF INVENTION: Tissue Metabolism.
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Dana-Farber Cancer Institute
; STREET: 44 Binney Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02115
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1 MB storage
; COMPUTER: IBM-compatible Compaq Prolinea MT 4/66
; OPERATING SYSTEM: MS/DOS
; SOFTWARE: Wordperfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/771,022F
; FILING DATE: 07-OCT-1991
; CLASSIFICATION: 800
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/589,971
; FILING DATE: 28-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: HART, JULIA D.
; REGISTRATION NUMBER: 33132
; REFERENCE/DOCKET NUMBER: DFCI-117
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 632-4016
; TELEFAX: (617) 632-4012
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE:
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; STRAIN: Swiss Webster
; DEVELOPMENTAL STAGE: embryonic
; TISSUE TYPE: embryonic fibroblast
; CELL TYPE: fibroblast
; CELL LINE: 3T3-F442A
; IMMEDIATE SOURCE:

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CLONE: ap2911  
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NAME/KEY: ARE7-containing nucleotide sequence  
LOCATION: 29 - 41  
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OTHER INFORMATION: are the nucleotides on  
OTHER INFORMATION: the coding strand of the mouse ap2 gene that are complementary  
OTHER INFORMATION: nucleotides 9 - 19 of SEQ ID  
OTHER INFORMATION: NO 9, which are on the non-coding strand of the mouse ap2 gene  
PUBLICATION INFORMATION:  
AUTHORS: GRAVES, REED A.  
AUTHORS: TONTONIZ, PETER  
AUTHORS: SPEIGELMAN, BRUCE M.  
TITLE: Analysis of a Tissue-Specific Enhancer: ARF6  
TITLE: Regulated Adipogenic Gene Expression  
JOURNAL: Molecular and Cellular Biology  
VOLUME: 12  
PAGES: 1202-1208  
DATE: 00-MAR-1992  
US-07-771-022F-16

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RESULT 5  
US-09-268-992-7/c  
Sequence 7, Application US/09268992  
Patent No. 6342351  
GENERAL INFORMATION:  
APPLICANT: Chen, H.  
APPLICANT: Frelmer, N.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS  
FILE REFERENCE: 7853-138  
CURRENT APPLICATION NUMBER: US/09/268,992  
CURRENT FILING DATE: 1999-03-16  
EARLIER APPLICATION NUMBER: 09/236,134  
EARLIER FILING DATE: 1999-01-22  
EARLIER APPLICATION NUMBER: 60/106,056  
EARLIER FILING DATE: 1998-10-28  
EARLIER APPLICATION NUMBER: 60/088,312  
EARLIER FILING DATE: 1998-06-05  
EARLIER APPLICATION NUMBER: 60/078,044  
EARLIER FILING DATE: 1998-03-16  
NUMBER OF SEQ ID NOS: 84  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 7  
LENGTH: 72604  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: all n positions  
OTHER INFORMATION: n=a, c, g, or t  
US-09-268-992-7

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Matches 91; Conservative 0; Mismatches 84;

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RESULT 6  
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Sequence 1, Application US/08261822A  
Patent No. 5650553  
GENERAL INFORMATION:  
APPLICANT: Ecker, Joseph R. et al.  
TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene  
TITLE OF INVENTION: and Pathogens  
NUMBER OF SEQUENCES: 82  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5650553r1s  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/261,822A  
FILING DATE: 17-JUN-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Beardell, Lori Y.  
REGISTRATION NUMBER: 34,293  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6042 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-261-822A-1

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Best Local Similarity 56.0%; Pred. No. 0.016; Indels 0; Gaps 0;  
Matches 75; Conservative 0; Mismatches 59;

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QY 399 tttgtctctctctgtcgaacctctctctgtatataatgcctctcaggtttctctctga 458  
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DB 178 CTCTATCTCTATCTCTCTGCTAGCTTGATAAGAGTCTTTCTTTTGAAGATCGTTTCTCT 237  
QY 459 atcatctctgtga 472  
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DB 238 CTCTCTCACTGAGA 251

RESULT 7  
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Sequence 1, Application PC/TUS9507744A  
GENERAL INFORMATION:



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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,288
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Beardell, Lori Y.
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: UPN-2949
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6172 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
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US-09-400-348-1
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Best Local Similarity 56.0% Pred. No. 0.017;
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Db 250 TCTTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 309
QY 399 tttgtctctctctgtcctaaccctccctcgatatatgcctctcaggtttcattctga 458
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QY 459 atcatctactgtga 472
Db 370 CTCTCTCACTGAGA 383

RESULT 10
US-09-007-005-17/c
; Sequence 17, Application US/09007005B
; Patent No. 6258558
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350003
; CURRENT APPLICATION NUMBER: US/09/007,005B
; CURRENT FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 289
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
;
US-09-007-005-17
Query Match 7.5% Score 38.8; DB 4; Length 289;
Best Local Similarity 9.6% Pred. No. 0.0068;

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Db      190   CCTCTTCCCTTCCTTCCCTTCCTTTTGACA    232
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RESULT          13  
US-09-128-156 : Sequence 16, Application US/09128155  
                ; Patent No. 6117654  
                ; GENERAL INFORMATION:
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, APPLICATION: PAB1, 1494
,
, TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
,
, TITLE OF INVENTION: AND USES THEREOF
,
, FILE REFERENCE: 09404/052001
,
, CURRENT APPLICATION NUMBER: US/09/128,155
,
, CURRENT FILING DATE: 1998-08-03
,
, EARLIER APPLICATION NUMBER: US 60/091,650
,
, EARLIER FILING DATE: 1998-07-02
,
, EARLIER APPLICATION NUMBER: US 60/054,646
,
, EARLIER FILING DATE: 1997-08-04
,
, NUMBER OF SEQ ID NOS: 18
,
, SOFTWARE: FastSeq for Windows Version 3.0
,
, SEQ ID NO 16
,
, LENGTH: 152331

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; SOFTWARE.
; SEQ ID NO 1
; LENGTH: 1
; TYPE: DNA
; ORGANISM:
; FEATURE:
; NAME/KEY:
; LOCATION:

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US-09-128-155-16

US-09-128-155-16

Query Match	7.4%	Score 38.2;	DB 3;	Length 152331.
Best Local Similarity	50.3%;	Pred. No. 0.21;		
Matches 94;	Conservative	0;	Mismatches 93;	Indels 0;

Query Match (7.4%) Score (50.2) DE (3) Length (32332)  
Best Local Similarity 50.3% Pred. No. 0.21;  
Matches 94: Conservative 0: Mismatches 93: Indels 0: Gaps 0:

[illegible]

Qy 329 cttctatggctcccttttctgtgattttcatggtttctgagctcttttccccgctttat 388

[illegible]

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QY 389 gattttctctttttgtctctctctgctaaccctccttcgtatatatgccccctcaggt 448

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Qy 449 tcatttctgaatcatctactgtgaactattcccattgtttgccagaagccccctggttct 508

Dd 128622 ctctctttctcttctcttctcttctctccctcctctctcttct 128681

Qy 509 tccttct 515  
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120600 + + + + + 120600

889871 333333 299871 00

## RESULT 14

US-09-128-155-17

; Sequence 17, Application US/09128155

Patent No. 6117654

; GENERAL INFORMATION:

APPLICANT: Pan, Yang

TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

1. TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILIES

FILE REFERENCE: 09404/052001

7. CURRENT APPLICATION NUMBER: US/09/128,155

; CURRENT FILING DATE: 1998-08-03

; EARLIER APPLICATION NUMBER: US 60/091,650

; EARLIER FILING DATE: 1998-07-02

; EARLIER APPLICATION NUMBER: US 60/054,646  
 ; EARLIER FILING DATE: 1997-08-04

; EARLIER FILING DATE: 1997-08-04  
 ; NUMBER OF SEQ ID NOS: 18

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; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0

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, SOFTWARE: FASTSEE FOR WINDOWS VERSION 3.0
: SEO ID NO 17

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LENGTH: 176373

TYPE: DNA

; ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(176373)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17

Query Match      7.4%; Score 38.2; DB 3; Length 176373;
Best Local Similarity 50.3%; Pred. No. 0.22;
Matches 94; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 329 ctctatggtccctttctgtgatttcatggtttctgagctcttttcccccgctttat 388
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Db 144525 ctctctctctctctctctctctctctctctctctctctctctctctctctct 144584

QY 389 gattttctcttttctctctctctctgctaaacctctctgtatataatgacctctcaggtt 448
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 144585 ttctttctctctctctctctctctctctctctctctctctctctctctctctct 144644

QY 449 tcattctgaatactactgtgaaactatctccattgtttgcccagaagccccctggtct 508
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 144645 ctctctctctctctctctctctctctctctctctctctctctctctctctctct 144704

QY 509 tctctct 515
      |||||
Db 144705 ttctttt 144711
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RESULT 15
US-08-929-329-1/c
; Sequence 1, Application US/08929329
; Patent No. 6120770
; GENERAL INFORMATION:
; APPLICANT: Adams, John H
; APPLICANT: Dalton, John P
; APPLICANT: Kappe, Stefan
; TITLE OF INVENTION: Plasmodium Proteins Useful for Preparing
; TITLE OF INVENTION: Vaccine Compositions
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnes & Thornburg
; STREET: 11 S Meridian
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/929.329
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Breen, John P
; REGISTRATION NUMBER: 38,833
; REFERENCE/DOCKET NUMBER: 835910-28685
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 231-7745
; TELEFAX: (317) 231-7433
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5433 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium yoelii
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US-08-929-329-1

Query Match 7.1%; Score 36.6; DB 3; Length 5433;  
Best Local Similarity 47.2%; Pred. No. 0.13;  
Matches 111; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 279 tcgcctctctctctctctgttgaggggttgagccactgtggcctgagcgacttctatggc 338  
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Db 3730 TTCTCTTCTGCTTTTTCAGCTTCTTCAATTCGTTTTCTTCTTCTTCTGCTTCTTTCG 3671

QY 339 tcccttttctgtgatttctcatggtttctgagctcttttcccccgctttatgatctctet 398  
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Db 3670 AGCTTCAATTAATTTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3611

QY 399 ttttctctctctctctgctaaacctctctgctatatatgacctctcaggtttctatctga 458  
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QY 459 atcatctactgtgaactattccccattgtttgcccagaagccccctggtttctctct 513  
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Search completed: June 8, 2002, 09:35:02  
Job time: 5850 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 8, 2002, 09:40:18 ; Search time 369.19 Seconds  
(without alignments)  
2408.954 Million cell updates/sec

Title: US-09-503-596-8  
Perfect score: 518  
Sequence: 1 gaattccagcaggaatcagg.....ccctgggtctctctcttaga 518

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	518	100.0	518	17 AAT08982	Adipose specific e
2	518	100.0	518	21 AAA37718	Mouse AFABP enhanc
3	508.8	98.2	512	13 AAO23906	Adipose specific e
C 4	41	7.9	13076	22 AAL06214	Human reproductive
C 5	41	7.9	13076	22 AAL07355	Human reproductive
C 6	40.6	7.8	72604	20 AAZ10752	Genomic sequence o
7	39.6	7.6	6042	17 AAT09018	Arabidopsis thalia
8	39.6	7.6	6172	19 AAV57454	Arabidopsis ethyle
9	39.6	7.6	6172	22 AAD03789	Arabidopsis thalia

C 10	39.4	7.6	4590	22 AAH24065	Yeast AOB9604-asso
11	39.4	7.6	15484	22 AAH70808	Human immune/haema
12	39.2	7.6	2010	10 AAN91379	Intron 1 from huma
C 13	39	7.5	80331	22 AAC89559	Human histone deac
C 14	38.6	7.5	2118	22 AAD16391	Mouse interferon i
C 15	38.4	7.4	857	23 AAS92392	DNA encoding novel
16	38.2	7.4	372	20 AAZ27713	Human DNA marker c
17	38.2	7.4	5059	20 AAH84332	Stealth virus nucl
18	38.2	7.4	10620	20 AAX02996	Human IL-1ra BAC c
19	38.2	7.4	14690	20 AAX22303	Human IL-1ra BAC c
20	37.6	7.3	1020	22 AAF63569	Murine phosphatase
C 21	37.6	7.3	1520	22 AAI90669	Human polynucleoti
C 22	37.4	7.2	2347	23 AAS75464	DNA encoding novel
C 23	37.4	7.2	2482	23 AAS90736	DNA encoding novel
C 24	37.4	7.2	6644	22 AAF31479	ZALPHA associated
C 25	37.4	7.2	9539	22 AAS45346	Chemically pretrea
C 26	37	7.1	1466	24 AAS63068	Cell death protect
27	36.8	7.1	887	22 AAI94062	Human neuroblastom
C 28	36.8	7.1	2315	21 AAF18129	Lung cancer associ
C 29	36.8	7.1	2337	22 AAH81742	Human differential
C 30	36.8	7.1	44453	20 AAX23519	Human kidney amino
31	36.8	7.1	49999	20 AAZ23891	Murine LOBO genomi
32	36.8	7.1	49999	20 AAZ23896	Murine LOBO homolo
C 33	36.6	7.1	567	22 AAH33915	Human colon cancer
C 34	36.6	7.1	5433	21 AAS99265	Plasmodium yoelii
C 35	36.4	7.0	139	24 AAS63092	Cell death protect
36	36.4	7.0	1001	21 AAH51571	Human 6PGD related
C 37	36.4	7.0	1239	23 AAS65580	DNA encoding novel
C 38	36.4	7.0	1239	23 AAS66695	DNA encoding novel
C 39	36.4	7.0	1239	23 AAS71706	DNA encoding novel
C 40	36.4	7.0	1717	23 AAS75833	DNA encoding novel
C 41	36.4	7.0	2043	23 AAS75793	DNA encoding novel
C 42	36.4	7.0	2389	18 AAT96470	MSRV-1 clone JLBcl
C 43	36.4	7.0	2389	19 AAV43161	Multiple sclerosis
C 44	36.4	7.0	5306	24 ABL32510	Human immune syste
45	36.4	7.0	34488	22 AAF97854	Human neuroblastom

# ALIGNMENTS

RESULT		1	
AAT08982		AAT08982	
ID	AAT08982 standard; DNA; 518 BP.		
XX	AAT08982;		
AC	11-JUL-1996 (first entry)		
DT	Adipose specific enhancer element.		
DE	Adipose; enhancer element; murine; adipocyte P2; gene; ap2;		
XX	lipolytic; lipogenic; protein; adipose tissue; recombinant;		
KW	metabolism; transgenic animal; fat tissue; homeostasis; disease;		
KW	obesity; study; ds.		
XX	Mus musculus.		
OS	XX		
XX	US5476926-A.		
PN	XX		
XX	19-DEC-1995.		
PD	XX		
XX	28-SEP-1990; 90US-0589971.		
PF	XX		
XX	07-OCT-1991; 91US-0771022.		
PR	28-SEP-1990; 90US-0589971.		
XX	(GRAV/) GRAVES R.		
PA	(ROSS/) ROSS S.		
PA	(SPIE/) SPIEGELMAN B M.		
PI	Graves R, Ross S, Spiegelman BM;		
XX			

DR WPI; 1996-049020/05.  
XX  
PT New murine adipose-specific enhancer element - used for fat-specific  
PT expression of a heterologous gene for production of a recombinant  
PT protein  
XX  
PS Claim 2; Columns 35-36; 46pp; English.  
XX  
CC The present sequence, an adipose specific enhancer element (ASEE),  
CC is derived from the 5'-flanking region of the murine adipocyte P2  
CC (aP2) gene. A DNA sequence comprising the ASEE linked through a  
CC functional promoter to a heterologous gene, which encodes a  
CC recombinant protein with a lipolytic or lipogenic effect on  
CC adipose tissue, is capable of specifically directing the in vivo  
CC expression of the protein in adipose tissue. The DNA can be used  
CC to exert an effect on adipose tissue metabolism, and in the  
CC prodn. of transgenic animals which exhibit altered fat tissue  
CC metabolism. Such animals can be leaner or more obese, and can be  
CC used in the study of adipose homeostasis and disease states  
CC associated with adipose tissue, e.g. obesity.  
XX  
SQ Sequence 518 BP; 113 A; 146 C; 108 G; 151 T; 0 other;  
  
Query Match 100.0%; Score 518; DB 17; Length 518;  
Best Local Similarity 100.0%; Pred. No. 3.9e-144;  
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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DB 1 gaattccagcagaatcaggtagctggaatgcacagagccatcgattcttgcaag 60  
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DB 61 ccatgcgacaaaggcagaatgcacatttcacccagagagaaggattgatgcagcag 120  
QY 121 aagtcaccaccagagacaaatggattccacagatgcctgacattgcttctactgg 180  
DB 121 aagtcaccaccagagacaaatggattccacagatgcctgacattgcttctactgg 180  
QY 181 atcagagttcactagtggaagtgtcacagcccaaacactcccccaagctcagcccttc 240  
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QY 241 ttgccttgtaacaatacagccgctcctggaatgcctccgctctctctcttttgga 300  
DB 241 ttgccttgtaacaatacagccgctcctggaatgcctccgctctctctcttttgga 300  
QY 301 gggttgagccactgtggcctgagcagcttctatggtcccttttctgtgatttcag 360  
DB 301 gggttgagccactgtggcctgagcagcttctatggtcccttttctgtgatttcag 360  
QY 361 gttcttgagctcttttcccccgtttatgattttctcttttctctctctctctctaa 420  
DB 361 gttcttgagctcttttcccccgtttatgattttctcttttctctctctctctctaa 420  
QY 421 ctccttcgtatatagcctctcgaagtttcatttctgtaatactactgtgaactattcc 480  
DB 421 ctccttcgtatatagcctctcgaagtttcatttctgtaatactactgtgaactattcc 480  
QY 481 catgtgttgccagaagcccttggttctctctctctctctctctctctctctctctct 518  
DB 481 catgtgttgccagaagcccttggttctctctctctctctctctctctctctctctct 518  
  
RESULT 2  
ID AAA37718  
XX AAA37718 standard; cDNA; 518 BP.  
AC AAA37718;  
XX  
DT 22-NOV-2000 (first entry)  
XX

DE Mouse AFABP enhancer sequence.  
XX  
KW AFABP; adipocyte fatty acid binding protein; atherosclerotic lesion;  
KW lesion formation inhibition; macrophage; adipocyte; atherosclerosis;  
KW serum cholesterol; therapy; mouse; enhancer; ss.  
XX  
OS Mus sp.  
XX  
PN WO200047734-A1.  
XX 17-AUG-2000.  
XX  
PF 11-FEB-2000; 2000WO-US03560.  
XX  
PR 12-FEB-1999; 99US-0119880.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Lee M, Perrella MA, Hotamisligil GS;  
XX WPI; 2000-506094/45.  
XX  
XX Reducing expression of adipocyte fatty acid binding protein through  
PT administration of a compound is used to inhibit formation of an  
PT atherosclerotic lesion -  
XX  
PS Disclosure; Page 18; 43pp; English.  
XX  
CC This sequence is the mouse AFABP (adipocyte fatty acid binding  
CC protein) enhancer sequence. The invention relates to a method  
CC for inhibiting formation of an atherosclerotic lesion comprising  
CC administering to a mammal a compound that reduces expression of adipocyte  
CC fatty acid binding protein (AFABP). The method is used to inhibit  
CC formation of atherosclerotic lesions. The method is used to identify  
CC compounds which can be used to inhibit formation of atherosclerotic  
CC lesions through inhibition of AFABP binding to an intracellular ligand  
CC in a macrophage or adipocyte, inhibition of development of an  
CC atherosclerotic lesion, inhibition of a macrophage differentiating into  
CC a foam cell or inhibition of AFABP expression in a cell. AFABP activity  
CC may be inhibited to treat atherosclerosis or to treat individuals at risk  
CC of developing atherosclerosis. Inhibiting AFABP expression or activity  
CC reduces the development of atherosclerotic lesions despite a high level  
CC of serum cholesterol.  
XX  
SQ Sequence 518 BP; 113 A; 146 C; 108 G; 151 T; 0 other;  
  
Query Match 100.0%; Score 518; DB 21; Length 518;  
Best Local Similarity 100.0%; Pred. No. 3.9e-144;  
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 gaattccagcagaatcaggtagctggaatgcacagagccatcgattcttgcaag 60  
DB 1 gaattccagcagaatcaggtagctggaatgcacagagccatcgattcttgcaag 60  
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DB 61 ccatgcgacaaaggcagaatgcacatttcacccagagagaaggattgatgcagcag 120  
QY 121 aagtcaccaccagagacaaatggattccacagatgcctgacattgcttctactgg 180  
DB 121 aagtcaccaccagagacaaatggattccacagatgcctgacattgcttctactgg 180  
QY 181 atcagagttcactagtggaagtgtcacagcccaaacactcccccaagctcagcccttc 240  
DB 181 atcagagttcactagtggaagtgtcacagcccaaacactcccccaagctcagcccttc 240  
QY 241 ttgccttgtaacaatacagccgctcctggaatgcctccgctctctctcttttgga 300  
DB 241 ttgccttgtaacaatacagccgctcctggaatgcctccgctctctctcttttgga 300  
QY 301 gggttgagccactgtggcctgagcagcttctatggtcccttttctgtgatttcag 360  
DB 301 gggttgagccactgtggcctgagcagcttctatggtcccttttctgtgatttcag 360

Db 301 ggggtggagccacactgtggcctgagcgactctctatgctccctcttctgtgattttcatg 360  
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Db 361 gtttctgagctcttttccccccgctttatgattttctctttttgtctctctcttctgtaaac 420  
QY 421 ctctctgtatataatgctctcaggtttcattttctgtgaatcactactgtgaactattcc 480  
Db 421 ctctctgtatataatgctctcaggtttcattttctgtgaatcactactgtgaactattcc 480  
QY 481 cattgtttccagaagccccctgggtttcttctctctaga 518  
Db 481 cattgtttccagaagccccctgggtttcttctctctaga 518  
RESULT 3  
AAQ23906  
ID AAQ23906 standard; DNA; 512 BP.  
XX  
XX  
AC AAQ23906;  
23-OCT-1992 (first entry)  
DE Adipose specific enhancer ap2.  
KW SV40; small t antigen; lipolytic; liogenic; ss.  
XX  
OS Mus musculus.  
XX  
XX WO9206104-A.  
XX  
PD 16-APR-1992.  
XX  
XX  
PF 25-SEP-1991; 91WO-US06989.  
XX  
XX 28-SEP-1990; 90US-0589971.  
XX  
PA (DANC ) DANA-FARBER CANCER.  
PA (UNII ) UNIV OF ILLINOIS COLLEGE.  
XX  
PI Graves R, Ross S, Spiegelman BM;  
XX  
XX WPI; 1992-150807/18.  
XX  
PT Adipocyte-specific enhancers and promoters - for prodn. of  
PT transgenic animals exhibiting altered fat metabolism  
XX  
PS Disclosure; Page 77; 103pp; English.  
XX  
CC The sequence given encodes an adipose-specific enhancer, ap2, which,  
CC within the scope of the invention, can be operatively linked to a DNA  
CC coding sequence for a recombinant protein having either a lipolytic or  
CC lipogenic effect on adipose tissue. This transgene was transfected  
CC into mice. The DNA coding sequence used was a 280 bp fragment of the  
CC SV40 small t antigen splice/polyadenylation sequences.  
XX  
SQ Sequence 512 BP; 110 A; 146 C; 107 G; 149 T; 0 other;  
Query Match 98.2%; Score 508.8; DB 13; Length 512;  
Best Local Similarity 99.6%; Pred. No. 2.1e-141;  
Matches 510; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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Db 1 ccagcagggaatcaggtagctgggaatcgacagagccatcgattcttggcagccatg 60  
QY 66 cgacaaaggcagaatgcacatttcacacagagagagagggatgatgcagcgggaagtc 125  
Db 61 cgacaaaggcagaatgcacatttcacacagagagagagggatgatgcagcgggaagtc 120  
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Db 121 accaccacagagcaaatggaggttccacagatgaccttgccttcttcttactggatcag 180  
QY 186 agttcactagtgaaagtgtcacagcccaaacactccccaaagctcagcccttctctgccc 245  
Db 181 agttcactagtgaaagtgtcacagcccaaacactccccaaagctcagcccttctctgccc 240  
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Db 301 ggagcccaactgtgctgagcgacttctatgctcccttttctgtgattttcatggttcc 360  
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Db 361 tgagctcttttcccccgctttatgattttctcttctgtctctctctgtgtaaacctct 420  
QY 426 tegtatatatgcccctctcaggtttcattttctgaatcactactgaactattcccatg 485  
Db 421 tegtatatatgcccctctcaggtttcattttctgaatcactactgaactattcccatg 480  
QY 486 ttgcccagaagccccctgggtttcttctctctag 517  
Db 481 ttgcccagaagccccctgggtttcttctctctag 512  
RESULT 4  
AAL06214/C  
ID AAL06214 standard; DNA; 13076 BP.  
XX  
AC AAL06214;  
XX  
DT 21-NOV-2001 (first entry)  
DE Human reproductive system related antigen DNA SEQ ID NO: 8902.  
XX  
KW Human; reproductive system related antigen; reproductive system disorder;  
KW cancer; gene therapy; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200155320-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US01339.  
XX  
PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.

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ID	AAAL07355	standard; DNA; 13076 BP.	
XX	XX		
AC	AAAL07355;		
XX	XX		
DT	21-NOV-2001	(first entry)	
XX	XX		
DE	Human reproductive system related antigen DNA SEQ ID NO: 10043.		
XX	XX		
KW	Human; reproductive system related antigen; reproductive system disorder;		
KW	cancer; gene therapy; ds.		
OS	Homo sapiens.		
XX	XX		
PN	WO200155320-A2.		
XX	XX		
	02-AUG-2001.		
	17-JAN-2001;	2001WO-US01339.	
XX	XX		
PR	31-JAN-2000;	2000US-0179065.	08-SEP-2000; 2000US-0232080.
PR	04-FEB-2000;	2000US-0180628.	08-SEP-2000; 2000US-0232081.
PR	24-FEB-2000;	2000US-0184664.	12-SEP-2000; 2000US-0231968.
PR	02-MAR-2000;	2000US-0186350.	PR 14-SEP-2000; 2000US-0232397.
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PR	19-MAY-2000;	2000US-0205515.	PR 14-SEP-2000; 2000US-0234401.
PR	07-JUN-2000;	2000US-0209467.	PR 14-SEP-2000; 2000US-0233063.
PR	28-JUN-2000;	2000US-0214886.	PR 14-SEP-2000; 2000US-0233064.
PR	30-JUN-2000;	2000US-0215135.	PR 14-SEP-2000; 2000US-0233065.
PR	07-JUL-2000;	2000US-0216647.	PR 21-SEP-2000; 2000US-0234223.
PR	17-JUL-2000;	2000US-0216880.	PR 21-SEP-2000; 2000US-0234224.
PR	11-JUL-2000;	2000US-0217487.	PR 21-SEP-2000; 2000US-0234274.
PR	11-JUL-2000;	2000US-0217496.	PR 25-SEP-2000; 2000US-0234997.
PR	14-JUL-2000;	2000US-0218290.	PR 25-SEP-2000; 2000US-0234998.
PR	26-JUL-2000;	2000US-0220963.	PR 26-SEP-2000; 2000US-0235484.
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PR	14-AUG-2000;	2000US-0225268.	PR 02-OCT-2000; 2000US-0236802.
PR	14-AUG-2000;	2000US-0225270.	PR 02-OCT-2000; 2000US-0237037.
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PR	14-AUG-2000;	2000US-0225757.	PR 02-OCT-2000; 2000US-0237039.
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PR	14-AUG-2000;	2000US-0225759.	PR 13-OCT-2000; 2000US-0239935.
PR	18-AUG-2000;	2000US-0226279.	PR 13-OCT-2000; 2000US-0239937.
PR	22-AUG-2000;	2000US-0226681.	PR 20-OCT-2000; 2000US-0240960.
PR	22-AUG-2000;	2000US-0226686.	PR 20-OCT-2000; 2000US-0241221.
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PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
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PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
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PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Rosen CA, Barash SC, Ruben SM;  
XX WPI; 2001-483426/52.  
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
XX useful for preventing, diagnosing and/or treating cancers and  
XX metastasis -  
XX Disclosure; SEQ ID NO 25620; 3071pp + Sequence Listing; English.  
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)  
XX amino acid sequences given in AAM82170 to AAM91921. (I) have cystostatic  
CC







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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 8, 2002, 08:43:34 ; Search time 2258.96 Seconds  
(without alignments)  
4798.644 Million cell updates/sec

Title: us-09-503-596-8  
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Scoring table: IDENTITY\_NUC  
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Searched: 1797656 seqs, 10463268293 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	74.2	14.3	7218	6	I66494	I66494 Sequence 14
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9	47	9.1	192381	2	AC107311	AC107311 Homo sapi
10	46.2	8.9	174742	9	AC068102	AC068102 Homo sapi
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12	45.8	8.8	56509	2	AC099974	AC099974 Mus muscu
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18	44.4	8.6	219424	2	AC110011	AC110011 Homo sapi
19	44.4	8.6	309401	2	AC016584	AC016584 Homo sapi
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ALIGNMENTS

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DEFINITION	Sequence 1 from patent US 5476926.						
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VERSION	I16725.1						
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unclassified.						
REFERENCE	1 (bases 1 to 518)						
AUTHORS	Spiegelman,B.M., Graves,R. and Ross,S.						
TITLE	Adipocyte-specific DNA sequences and use thereof in the production of transgenic animals exhibiting altered fat tissue metabolism						
JOURNAL	Patent: US 5476926-A 1 19-DEC-1995;						
FEATURES	Location/Qualifiers						
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## RESULT 2

MUSAP2A MUSAP2A 518 bp DNA linear ROD 27-APR-1993  
LOCUS Mus musculus fatty acid binding protein (ap2) gene, enhancer.

ACCESSION M84651

VERSION M84651.1 GI:191984

KEYWORDS adipocyte P2; fatty acid binding protein.

SOURCE Mus musculus (strain Swiss) DNA.

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 518)

AUTHORS Graves, R.A., Tontoz, P. and Spiegelman, B.M.

TITLE Analysis of a tissue-specific enhancer: ARF6 regulates adipogenic

gene expression

JOURNAL Mol. Cell. Biol. 12, 1202-1208 (1992)

MEDLINE 9218651

FEATURES Location/Qualifiers

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/strain="Swiss"

/db\_xref="taxon:10090"

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Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 481 catgtttgcccagaagccccctggttctctctctctctctctctctctctctctctctct 518  
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## RESULT 3

AC018616 AC018616 165948 bp DNA linear PRI 30-MAY-2001  
LOCUS Homo sapiens chromosome 8, clone RP11-15714, complete sequence.

ACCESSION AC018616

VERSION AC018616.5 GI:14249085

KEYWORDS HTG.

SOURCE human.

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 165948)

AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.

TITLE Homo sapiens chromosome 8, clone RP11-15714

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 165948)

AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Bada, F.,

Boguslavsky, I., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,

Choepe, Y., Collangelo, M., Collins, S., Collymore, A., Cooke, P.,

Dearellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J.,

Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,

Gardyna, S., Grant, G., Hagos, B., Hearford, A., Horton, L.,

Howland, J., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

Landers, T., Lechoczky, J., Levine, R., Liu, C., Liu, G., Locke, K.,

Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,

Meldrum, J., Meneus, L., Morrow, J., Naylor, J., Norman, C. H.,

O'Connor, T., O'Donnell, P., Olivari, T. M., Peterson, K., Pierre, N.,

Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A.,

Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,

Subramanian, A., Talamas, J., Testfaye, S., Theodore, J., Tirrell, A.,

Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Zimmer, A.

and Zody, M.

Direct Submission

Submitted (14-DEC-1999) Whitehead Institute/MIT Center for Genome

## TITLE

## JOURNAL



REFERENCE AUTHORS	Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 165948) Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Karatas,A., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G., MacLean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M., McSwan,P., McKernan,K., McPheters,R., Meldrim,J., Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P., Sougnuez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zemбек,L., Zimmer,A. and Zody,M.
TITLE JOURNAL	Direct Submission Submitted (30-MAY-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT	On May 30, 2001 this sequence version replaced gi:12331511. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html ----- Genome Center Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu ----- Project Information Center project name: L5176 Center clone name: 157_I_4 -----
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Qy 311 ccaact 315
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LOCUS I66494 7218 bp DNA linear PAT 28-DEC-1997
DEFINITION Sequence 14 from patent US 5670367.
ACCESSION I66494
VERSION I66494.1 GI:2724471
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 7218)
AUTHORS Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.
TITLE Recombinant fowlpox virus
JOURNAL Patent: US 5670367-A 14 23-SEP-1997;
FEATURES
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Qy 203 gtcacagcccaaacactccccaaagctcagccctctctgcttctgttaacaatcaagcg 262
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Db 1164 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1223
Qy 323 gagcactctatggtccctcttctgtgatttctatggttctctgagctcttttccccc 382
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DEFINITION STS 8,3640F, sequence tagged site.
ACCESSION G32180
VERSION G32180.1 GI:2198618
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE human Flow sorted human chromosome 8 from hamster (CHO)/ human lymphocyte UV20HL21-17 hybrid. Library designated LL08NS02--from Lawrence Livermore Laboratory.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 507)
AUTHORS Pierce,J., Naylor,S.L., He,X., Sardaar,R., Gonzales,O., Gilliam,B., Morrish,T., Pekkel,V., Reus,B.E., Leach,R.J. and O'Connell,P.
TITLE Framework Hybrid Mapping of Chromosome 8: Assignment of 361 STS Markers to Cytogenetic Bins and Definition of Cytogenetic Breakpoints on the Genethon Genetic Map
JOURNAL Unpublished
COMMENT
Contact: Peter O'Connell, Ph.D.
Department of Pathology
University of Texas Health Science Center at San Antonio
7703 Floyd Curl Drive San Antonio, TX 78284, USA
Tel: (210)567-4126
Fax: (210)567-6729
Email: oconnell@uthscsa.edu
Primer A: CAAAAGTGCTCCCGAGAAAG
Primer B: GATAGCAGCAGATGCCACAA
STS size: 132.
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Matches 170; Conservative 0; Mismatches 69; Indels 7; Gaps 5;
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[illegible]







Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S.,  
Severy, P., Sougnès, C., Spencer, B., Stange-Thomann, N.,  
Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S.,  
Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,  
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,  
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

# Direct Submission

Submitted (29-MAY-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 174742)

## REFERENCE

### AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,  
Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B.,  
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,  
Choepel, Y., Colangelo, M., Collins, S., Collamore, A., Cook, A.,  
Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S.,  
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Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,  
Hagos, B., Heard, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,  
Jones, C., Kamat, A., Karatas, A., Kells, C., LaRoque, K.,  
Lamazares, R., Landers, T., Lehoczký, J., Levine, R., Liu, G.,  
MacLean, C., MacDonald, P., Major, J., Marquis, N., Matthews, C.,  
McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J.,  
Mense, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C.,  
Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D.,  
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,  
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,  
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,  
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Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,  
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,  
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,  
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

## Direct Submission

Submitted (10-DEC-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA

On Dec 10, 2001 this sequence version replaced gi:14211833.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence\_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L7452

Center clone name: 333\_M\_8

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## FEATURES

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Location/Qualifiers

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AC099974.1 GI:17047340  
HTG: HTGS\_PHASE0.  
house mouse.  
Mus musculus  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
Mus musculus, clone RP23-22J3  
Unpublished  
2 (bases 1 to 56509)  
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,  
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,  
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Choepe,Y., Collangelo,M., Collins,S., Collymore,A., Cook,A.,  
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,  
Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,  
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,  
Jones,B., Heatford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,  
Jonges,C., Kamat,A., Karatas,A., Kells,C., Lakocque,K.,  
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,  
MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,  
McCarthy,M., McEwan,P., McKernan,K., MCPheeters,R., Meldrim,J.,  
Meneus,L., Mihova,T., Mienda,V., Murphy,T., Naylor,J., Nguyen,C.,  
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,  
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,  
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,  
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,  
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,  
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,  
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,  
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,  
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L13695  
Center clone name: 22\_J3  
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\* NOTE: This record contains 70 individual

\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 711: contig of 711 bp in length  
\* 712 811: gap of 100 bp  
\* 812 1512: contig of 701 bp in length  
\* 1513 1612: gap of 100 bp  
\* 1613 2331: contig of 719 bp in length  
\* 2332 2431: gap of 100 bp  
\* 2432 3145: contig of 714 bp in length  
\* 3146 3245: gap of 100 bp  
\* 3246 3958: contig of 713 bp in length  
\* 3959 4058: gap of 100 bp  
\* 4059 4781: contig of 723 bp in length  
\* 4782 4881: gap of 100 bp  
\* 4882 5584: contig of 703 bp in length  
\* 5585 5684: gap of 100 bp  
\* 5685 6396: contig of 712 bp in length  
\* 6397 6496: gap of 100 bp  
\* 6497 7281: contig of 785 bp in length  
\* 7282 7381: gap of 100 bp  
\* 7382 8058: contig of 677 bp in length  
\* 8059 8158: gap of 100 bp  
\* 8159 8868: contig of 710 bp in length  
\* 8869 8968: gap of 100 bp  
\* 8969 9682: contig of 714 bp in length  
\* 9683 9782: gap of 100 bp  
\* 9783 10496: contig of 714 bp in length  
\* 10497 10596: gap of 100 bp  
\* 10597 11305: contig of 709 bp in length  
\* 11306 11405: gap of 100 bp  
\* 11406 12093: contig of 688 bp in length  
\* 12094 12193: gap of 100 bp  
\* 12194 12887: contig of 694 bp in length  
\* 12888 12987: gap of 100 bp  
\* 12988 13703: contig of 716 bp in length  
\* 13704 13803: gap of 100 bp  
\* 13804 14517: contig of 714 bp in length  
\* 14518 14617: gap of 100 bp  
\* 14618 15337: contig of 720 bp in length  
\* 15338 15437: gap of 100 bp  
\* 15438 16140: contig of 703 bp in length  
\* 16141 16240: gap of 100 bp  
\* 16241 16950: contig of 710 bp in length  
\* 16951 17050: gap of 100 bp  
\* 17051 17768: contig of 718 bp in length  
\* 17769 17868: gap of 100 bp  
\* 17869 18584: contig of 716 bp in length  
\* 18585 18684: gap of 100 bp  
\* 18685 19395: contig of 711 bp in length  
\* 19396 19495: gap of 100 bp  
\* 19496 20179: contig of 684 bp in length  
\* 20180 20279: gap of 100 bp  
\* 20280 20965: contig of 686 bp in length  
\* 20966 21065: gap of 100 bp  
\* 21066 21774: contig of 709 bp in length  
\* 21775 21874: gap of 100 bp  
\* 21875 22572: contig of 698 bp in length  
\* 22573 22672: gap of 100 bp  
\* 22673 23396: contig of 724 bp in length  
\* 23397 23496: gap of 100 bp  
\* 23497 24326: contig of 830 bp in length  
\* 24327 24426: gap of 100 bp  
\* 24427 25144: contig of 718 bp in length  
\* 25145 25244: gap of 100 bp  
\* 25245 25945: contig of 701 bp in length

\* 25946 26045: gap of 100 bp  
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\* 26751 26850: gap of 100 bp  
\* 26851 27562: contig of 712 bp in length  
\* 27563 27662: gap of 100 bp  
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\* 28308 28407: gap of 100 bp  
\* 28408 29118: contig of 711 bp in length  
\* 29119 29218: gap of 100 bp  
\* 29219 29929: contig of 711 bp in length  
\* 29930 30029: gap of 100 bp  
\* 30030 30754: contig of 725 bp in length  
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\* 35609 35708: gap of 100 bp  
\* 35709 36375: contig of 667 bp in length  
\* 36376 36475: gap of 100 bp  
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\* 37173 37272: gap of 100 bp  
\* 37273 37985: contig of 713 bp in length  
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\* 38770 38869: gap of 100 bp  
\* 38870 39570: contig of 701 bp in length  
\* 39571 39670: gap of 100 bp  
\* 39671 40376: contig of 706 bp in length  
\* 40377 40476: gap of 100 bp  
\* 40477 41186: contig of 710 bp in length  
\* 41187 41286: gap of 100 bp  
\* 41287 42000: contig of 714 bp in length  
\* 42001 42100: gap of 100 bp  
\* 42101 42799: contig of 699 bp in length  
\* 42800 42899: gap of 100 bp  
\* 42900 43620: contig of 721 bp in length  
\* 43621 43720: gap of 100 bp  
\* 43721 44444: contig of 724 bp in length  
\* 44445 44544: gap of 100 bp  
\* 44545 45257: contig of 713 bp in length  
\* 45258 45357: gap of 100 bp  
\* 45358 46065: contig of 708 bp in length  
\* 46066 46165: gap of 100 bp  
\* 46166 46863: contig of 698 bp in length  
\* 46864 46963: gap of 100 bp  
\* 46964 47676: contig of 713 bp in length  
\* 47677 47776: gap of 100 bp  
\* 47777 48474: contig of 698 bp in length  
\* 48475 48574: gap of 100 bp  
\* 48575 49272: contig of 698 bp in length  
\* 49273 49372: gap of 100 bp  
\* 49373 50085: contig of 713 bp in length  
\* 50086 50185: gap of 100 bp  
\* 50186 50897: contig of 712 bp in length  
\* 50898 50997: gap of 100 bp  
\* 50998 51682: contig of 685 bp in length  
\* 51683 51782: gap of 100 bp  
\* 51783 52537: contig of 755 bp in length  
\* 52538 52637: gap of 100 bp  
\* 52638 53339: contig of 702 bp in length  
\* 53340 53439: gap of 100 bp  
\* 53440 54135: contig of 696 bp in length  
\* 54136 54235: gap of 100 bp  
\* 54236 54913: contig of 678 bp in length  
\* 54914 55013: gap of 100 bp

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* 55014 55702: contig of 689 bp in length
* 55703 55802: gap of 100 bp

Query Match      8.8%; Score 45.8; DB 2; Length 56509;
Best Local Similarity 53.7%; Pred. No. 0.026;
Matches 95; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 342 cttttctgtgatttcattggtttctgagctcttttccccgcgtttatgattttctctttt 401
Db 6090 cttttctgtgatttcattggtttctgagctcttttccccgcgtttatgattttctctttt 6031

QY 402 tgtctctctctgttaaacctcttcgtatatatgcctctcagggttcattcttgaatc 461
Db 6030 tcttttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 5971

QY 462 atctactgtgaactattccattgtttgcccagaagccccctggtttcttctcttaga 518
Db 5970 tcttttctgagatgggtttcttctgtgtgagccctggcgatcctagaaactactctctaga 5914

RESULT 13
AL663072
LOCUS      248963 bp      DNA      linear      HTG 01-FEB-2002
DEFINITION Mus musculus chromosome X clone RP23-22J3, *** SEQUENCING IN
PROGRESS ***, in unordered pieces.
ACCESSION  AL663072
VERSION     AL663072.8 GI:18491423
KEYWORDS   HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE     Mus musculus
ORGANISM   house mouse.
REFERENCE  1 (sites)
AUTHORS    Howden,P.
JOURNAL    Direct Submission
COMMENT    Submitted (31-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Feb 4, 2002 this sequence version replaced gi:18476984.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: bm22J3
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 248349 bases at least Q40
Consensus quality: 248604 bases at least Q30
Consensus quality: 248705 bases at least Q20
Insert size: 248763; sum-of-contigs
Insert size: 248868; 2.0% error; agarose-fp
Quality coverage: 9.38x in Q20 bases; sum-of-contigs Quality
coverage: 9.46x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

FEATURES             Location/Qualifiers
     source           1..248963
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /chromosome="X"
                     /clone="RP23-22J3"
                     /clone_lib="RPCI-23"
                     1..129645
                     /note="assembly fragment:04132
                     fragment_chain:1"
                     129746..125400
                     /note="assembly_fragment:05296

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```

fragment_chain:1"
225501..248963
/note="assembly_fragment:01912
fragment_chain:1"
BASE COUNT 76690 a 51750 c 50560 g 69759 t 204 others
ORIGIN

Query Match      8.8%; Score 45.8; DB 2; Length 248963;
Best Local Similarity 53.7%; Pred. No. 0.029;
Matches 95; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 342 cttttctgtgatttcattggtttctgagctcttttccccgcgtttatgattttctctttt 401
Db 175161 cttttctgtgatttcattggtttctgagctcttttccccgcgtttatgattttctctttt 175220

QY 402 tgtctctctctgttaaacctcttcgtatatatgcctctcagggttcattcttgaatc 461
Db 175221 tcttttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 175280

QY 462 atctactgtgaactattccattgtttgcccagaagccccctggtttcttctcttaga 518
Db 175281 tcttttctgagatgggtttcttctgtgtgagccctggcgatcctagaaactactctctaga 175337

RESULT 14
AC097569
LOCUS      121788 bp      DNA      linear      HTG 20-DEC-2001
DEFINITION Rattus norvegicus clone CH230-67E3, *** SEQUENCING IN PROGRESS ***,
65 unordered pieces.
ACCESSION  AC097569
VERSION     AC097569.3 GI:17974367
KEYWORDS   HTG; HTGS_PHASE1.
SOURCE     Norway rat.
ORGANISM   Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE  1 (bases 1 to 121788)
AUTHORS    Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbara,J.,
Benton,J., Binage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
Hollins,B., Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mahoney,E., McLeod,M.P., Meador,M.,
Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S.,
Ogih,M., Okwuonu,G., Oragunye,N., Owiedo,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.,
Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoohtari,N.,
Sisson,I., Sodergren,E., Sonalike,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,

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Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R.,  
Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C.,  
Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S.,  
Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D.,  
Weinstock, G. and Gibbs, R.

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Unpublished  
2 (bases 1 to 121788)

Worley, K.C.

Direct Submission

Submitted (19-OCR-2001) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

On Dec 20, 2001 this sequence version replaced gi:17062605.

COMMENT

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)

----- Project Information

Center project name: G17Z

Center clone name: CH230-67E3

----- Summary Statistics

Assembly program: Phrap; version 0.990329First call to

findPhrapList

Consensus quality: 93320 bases at least Q40

Consensus quality: 102603 bases at least Q30

Consensus quality: 109123 bases at least Q20

Estimated insert size: 63172; sum-of-contigs estimation

Quality coverage: 0x in Q20 bases; agarose-fp estimation

Quality coverage: 0.8x in Q20 bases; sum-of-contigs estimation

-----

\* NOTE: Estimated insert size may differ from sequence length

\* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 65 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will

\* be preserved.

\* 1 6540: contig of 6540 bp in length

\* 6641 6640: gap of unknown length

\* 6641 10202: contig of 3562 bp in length

\* 10203 10302: gap of unknown length

\* 13903 13913: contig of 3611 bp in length

\* 13914 14013: gap of unknown length

\* 14014 16759: contig of 2746 bp in length

\* 16760 16859: gap of unknown length

\* 16860 20400: contig of 3541 bp in length

\* 20401 20500: gap of unknown length

\* 20501 22351: contig of 1851 bp in length

\* 22352 22451: gap of unknown length

\* 22452 25002: contig of 2551 bp in length

\* 25003 25102: gap of unknown length

\* 25103 27203: contig of 2101 bp in length

\* 27204 27303: gap of unknown length

\* 27304 30014: contig of 2711 bp in length

\* 30015 32339: contig of 2225 bp in length

\* 32340 32439: gap of unknown length

\* 32440 34411: contig of 1972 bp in length

\* 34412 34511: gap of unknown length

\* 34512 37116: contig of 2605 bp in length

\* 37117 37216: gap of unknown length

\* 37217 39412: contig of 2196 bp in length

\* 39413 39512: gap of unknown length

\* 39513 41595: contig of 2083 bp in length

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\* 41696 44635: contig of 2940 bp in length

\* 44636 44735: gap of unknown length

\* 44736 47198: contig of 2463 bp in length

\* 47199 47299: gap of unknown length

\* 47299 48680: gap of unknown length

\* 48680 50621: contig of 1842 bp in length

\* 50622 52803: contig of 2082 bp in length

\* 52804 52903: gap of unknown length

\* 52904 54588: contig of 1685 bp in length

47199

47299

48680

48780

50622

50722

52804

52904

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54689

55942

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57499

57599

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79215

80267

80367

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83504

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88168

89676

89776

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104048

47298: gap of unknown length

48679: contig of 1381 bp in length

48779: gap of unknown length

50621: contig of 1842 bp in length

50721: gap of unknown length

52803: contig of 2082 bp in length

52903: gap of unknown length

54588: contig of 1685 bp in length

54688: gap of unknown length

55941: contig of 1253 bp in length

55942: gap of unknown length

57498: contig of 1457 bp in length

57598: gap of unknown length

59373: contig of 1775 bp in length

59473: gap of unknown length

60760: contig of 1287 bp in length

60860: gap of unknown length

61944: contig of 1084 bp in length

62044: gap of unknown length

63496: contig of 1452 bp in length

63596: gap of unknown length

65186: contig of 1590 bp in length

65286: gap of unknown length

66626: contig of 1340 bp in length

66726: gap of unknown length

68371: contig of 1645 bp in length

68471: gap of unknown length

69962: contig of 1491 bp in length

69963: gap of unknown length

71864: contig of 1802 bp in length

71964: gap of unknown length

73645: contig of 1681 bp in length

73745: gap of unknown length

74800: contig of 1055 bp in length

74900: gap of unknown length

76754: contig of 1854 bp in length

76854: gap of unknown length

77870: contig of 1016 bp in length

77970: gap of unknown length

79214: contig of 1144 bp in length

79215: gap of unknown length

80266: contig of 1052 bp in length

80366: gap of unknown length

81995: contig of 1629 bp in length

82095: gap of unknown length

83503: contig of 1408 bp in length

83603: gap of unknown length

84837: contig of 1234 bp in length

84937: gap of unknown length

86327: contig of 1390 bp in length

86427: gap of unknown length

88067: contig of 1640 bp in length

88167: gap of unknown length

89675: contig of 1508 bp in length

89775: gap of unknown length

90812: contig of 1037 bp in length

90912: gap of unknown length

92400: contig of 1488 bp in length

92500: gap of unknown length

93625: contig of 1125 bp in length

93725: gap of unknown length

95247: contig of 1522 bp in length

95347: gap of unknown length

96716: contig of 1369 bp in length

96816: gap of unknown length

98631: contig of 1815 bp in length

98731: gap of unknown length

100983: contig of 2252 bp in length

101083: gap of unknown length

102243: contig of 1160 bp in length

102343: gap of unknown length

103948: contig of 1605 bp in length

104048: gap of unknown length



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* 89119 89218: gap of 100 bp
* 89219 100341: contig of 11123 bp in length
* 100342 100441: gap of 100 bp
* 100442 109823: contig of 9382 bp in length
* 109824 109924: gap of 100 bp
* 109924 118272: contig of 8349 bp in length
* 118273 118372: gap of 100 bp
* 118373 128451: contig of 10079 bp in length
* 128452 128552: gap of 100 bp
* 128552 138311: contig of 9760 bp in length
* 138312 138411: gap of 100 bp
* 138412 151032: contig of 12621 bp in length
* 151033 151132: gap of 100 bp
* 151133 168498: contig of 17366 bp in length
* 168499 168598: gap of 100 bp
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            1158. 2655
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            2756. 4142
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